Cell Regulatory Genes, Encoded Products, And Uses Related Thereto

1. Background of the Invention

Neoplasia is characterized by deregulated cell growth and division. Inevitably, molecular pathways controlling cell growth must interact with those regulating cell division. It was not until very recently, however, that experimental evidence became available to bring such connection to light. Cyclin A was found in association with the adenovirus oncoprotein E1A in virally transformed cells (Giordona *et al.* *Cell* 58:981 (1989); and Pines et al. *Nature* 346:760 (1990)). The cell-cycle gene implicated most strongly in oncogenesis thus far is the human cyclin D1. It was originally isolated through genetic complementation of yeast G_1 cyclin deficient strains (Xiong et al. *Cell* 65:691(1991); and Lew et al. *Cell* 66:1197 (1991)), as cellular genes whose transcription is stimulated by CSF-1 in murine macrophages (Matsushine *et al.* *Cell* 65:701 (1991)) and in the putative oncogene *PRAD1* rearranged in parathyroid tumors (Montokura et al. *Nature* 350:512 (1991).

However, the creation of a mutant onocogene is only one of the requirements needed for tumor formation; tumorigenesis appears to also require the additional inactivation of a second class of critical genes: the "anti-oncogenes" or "tumor-suppressing genes." Tumor suppressor genes are a family of genes that negatively regulate cell growth and are lost or inactivated in most cancers. In their natural state these genes act to suppress cell proliferation. Damage to such genes leads to a loss of this suppression, and thereby results in tumorigenesis. Thus, the deregulation of cell growth may be mediated by either the activation of oncogenes or the inactivation of tumor-suppressing genes (Weinberg, R.A., (Sept 1988) *Scientific Amer.* pp 44-51).

Oncogenes and tumor-suppressing genes have a basic distinguishing feature. The oncogenes identified thus far have arisen only in somatic cells, and thus have been incapable of transmitting their effects to the germ line of the host animal. In contrast, mutations in tumor-suppressing genes can be identified in germ line cells, and are thus transmissible to an animal's progeny.

The classic example of a hereditary cancer is retinoblastomas in children. The incidence of the retinoblastomas is determined by a tumor suppressor gene, the

retinoblastoma (RB) gene (Weinberg, R.A., (Sept 1988) *Scientific Amer.*pp 44-51; Hansen et al. (1988) *Trends Genet* 4:125-128). Individuals born with a lesion in one of the RB alleles are predisposed to early childhood development of retinoblastomas. Inactivation or mutation of the second RB allele in one of the somatic cells of these susceptible individuals appears to be the molecular event that leads to tumor formation (Caveneee et al. (1983) *Nature* 305:799-784; Friend et al. (1987) *PNAS* 84:9059-9063).

The RB tumor-suppressing gene has been localized onto human chromosome 13. The mutation may be readily transmitted through the germ line of afflicted individuals (Cavenee, et al. (1986) *New Engl. J. Med* 314:1201-1207). Individuals who have mutations in only one of the two naturally present alleles of this tumor-suppressing gene are predisposed to retinoblastoma. Inactivation of the second of the two alleles is, however, required for tumorigenesis (Knudson (1971) *PNAS* 68:820-823).

A second tumor-suppressing gene is the *p53* gene (Green (1989) *Cell* 56:1-3; Mowat et al (1985 *Nature* 314:633-636). The protein encoded by the *p53* gene is a nuclear protein that forms a stable complex with both the SV40 large T antigen and the adenovirus E1B 55 kd protein. The p53 gene product may be inactivated by binding to these proteins.

Based on cause and effect analysis of *p53* mutants, the functional role of *p53* as a "cell-cycle checkpoint", particularly with respect to controlling progression of a cell from G1 phase into S phase, has implicated *p53* as able to directly or indirectly affect cycle cyle machinery. The first firm evidence for a specific biochemical link between *p53* and the cell-cycle comes a finding that p53 apparently regulates expression of a second protein, p21, which inhibits cyclin-dependent kinases (CDKs) needed to drive cells through the cell-cycle, e.g. from G1 into S phase. For example, it has been demonstrated that non-viral transformation, such as resulting at least in part from a mutation of deletion of of the p53 tumor suppressor, can result in loss of p21 from cyclin/CDK complexes. As described by Xiong et al. (1993) *Nature* 366:701-704, induction of p21 in response to p53 represents a plausible mechanism for effecting cell-cycle arrest in response to DNA damage, and loss of p53 may deregulate growth by loss of the p21 cell-cycle inhibitor.

More recently, researchers discovered yet another tumor suppressing gene, p73, which closely resembles p53. Not only does this protein bear a strong structural identity with p53, it also possess similar functional attributes. For instance, this protein disclosed

the growth-inhibiting and apoptosis promoting effects, it triggered p21 production, suggesting thereby that it inhibited cell growth through the same pathway as that used by p53. Here, we describe the discovery of a novel family of cell regulatory genes, the p-63 family, which exhibits considerable sequence identity with p53 and and p73, and appears to possess similar functional attributes.

2. Summary of the Invention

The p53 tumor suppressor protein is involved in multiple central cellular processes, including transcription, DNA repair, genomic stability, senescence, cell cycle control and apoptosis. p53 is functionally inactivated by structural mutations, interaction with viral products, and endogenous cellular mechanisms in the majority of human cancers. In fact, the p53 protein is one of the most frequently mutated tumor suppressor to be identified in human cancers. More than 50% of primary human tumor cells over-express a variety of mutant p53 forms. p73 which shares considerable structural identity maps to chromosomal region 1p36, a region which is frequently deleted in neuroblastoma and other tumors.

Here we describe a third family of cell regulatory genes, encoding the *p63*-family of proteins which also demonstrate considerable structural or sequence identity to the DNA-binding, oligomerization, and transactivation domains of p53. *p63* differs from p53 in that multiple *p63* transcripts yielding six major protein products have been discovered by cDNA cloning. For example, the six major *p63* products are listed in Fig. 2 C. It was found that unlike p53, the *p63* gene encodes multiple isotypes with remarkably divergent abilities. For instance, p63 variants possessing the N-terminus, i.e., TAp63γ, showed strong transactivation and cell-death inducing abilities. TAp63γ transactivates p53 reporter genes and may induce apoptosis. In addition, it was found that the predominant *p63* isotypes in many epithelial tissues lack an acidic N-terminus corresponding to the transactivation domain of p53. p63 variants which lack the transactivation domain, i.e., ΔNp63α, ΔNp63γ, suppressed transactivation by both p53 and p63. Additionally, these variants lacking the N-terminus may possibly regulate growth and may play an essential role in the regenerative processes, particularly regeneration of epithelial tissue. In one aspect, the invention discloses that these truncated *p63* variants can act as dominant-negative agents towards transactivation by p53, thereby suggesting the possibility of physiological

interactions amongst members of the p53 family. Examples of these variants include the disclosed ΔN*p63*α and ΔN*p63*γ. Thus, in one embodiment, the *p63* family of cell-regulatory proteins are involved in the modulation of cell growth or regulate the growth phenotype of a cell.

One aspect of the invention features a substantially pure preparation of a cell regulatory protein, or a fragment thereof, the full-length form of the cell regulatory protein having an amino acid sequence at least 70% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence at least 80% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence at least 90% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence at least 95% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence identical to the amino acid sequence represented in one of SEQ ID Nos. 13-24. In a preferred embodiment: the fragment comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

In yet another embodiment, the fragment includes the DNA binding domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

The DNA binding domain of these nucleic acid transcripts are remarkably conserved. The six variants demonstrate 100% identity in this region and this domain also demonstrates considerable identity to the corresponding DNA-binding domains of p53 and p73. It was found that *p63* variants bound the target sequences which are bound by p53, for example, ΔNp63γ, p53, and Tap63α all yielded significant mobility shifts with three separate oligonucleotides, specifically, with a minimal p53 binding sequence, a p53 binding site in the p21 promoter WAF, and a mutant p53 binding site. Results of the assay are shown in Figure 25.

Another aspect of the present invention features a polypeptide, of the cell regulator protein family, which functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation. In a preferred embodiment: the subject cell regulator-protein specifically binds a target DNA or protein; e.g. specifically binds a target DNA; e.g. is reasonably expected to transactivate genes involved in cell cycle arrest, such as p21; interacts with the DNA repair and synthetic machinery, such as proliferating cellular nuclear antigen, GADD 45, or proteins modulating apoptosis. In a more preferred embodiment, the cell regulator-protein regulates aand/or modulates growth of an eukaryotic cell-cycle, e.g. a mammalian cell-cycle, e.g., a human cell-cycle; the cell regulator protein inhibits cell growth of a eukaryotic cell, e.g., a human cell; the tumor suppressor-protein inhibits progression of a eukaryotic cell from G1 phase into S phase, e.g., inhibits progression of a mammalian cell from G1 phase into S phase, e.g., inhibits progression of a human cell from G1 phase into S phase; the cell regulator-protein suppresses tumor growth, e.g. in a tumor cell, e.g. in a tumor cell having an unimpaired p53 or *p63* or p53-like protein checkpoint. Yet another aspect of the present invention concerns an immunogen comprising a cell regulator-protein of the present invention, or a fragment thereof, in an immunogenic preparation, the immunogen being capable of eliciting an immune response specific for the cell regulator-protein; e.g. a humoral response, e.g., an antibody response; e.g. a cellular response. Thus, in one embodiment, the p-63 family of cell-regulatory proteins are involved in the modulation of cell growth or regulate the growth phenotype of a cell.

Another aspect of the present invention features recombinant cell regulator-protein, or a fragment thereof, cell regulatory protein, or a fragment thereof, the full-length form of the cell regulatory genes protein having an amino acid sequence at least 70% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence at least 80% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence at least 90% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence at least 95% homologous to the amino acid sequence represented in one of SEQ ID Nos. 13-24; the polypeptide has an amino acid sequence identical to the amino acid sequence represented in one of SEQ ID Nos. 13-24.

In a preferred embodiment: the fragment comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

In yet another embodiment, the fragment includes the DNA binding domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

In yet another embodiment, the fragment includes the core domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the core domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the core domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24. The core domain extends from about amino acids "PQV" through about amino acid "HLLQ", for instance, in TAp63γ, this region extends from about amino acid 70 through about amino acid 409.

In a preferred embodiment, the recombinant cell regulator-protein functions in one of either role of an agonist of cell-cycle regulation or an antagonist of cell-cycle regulation. In a preferred embodiment: the subject p63 protein specifically binds a target DNA or protein; e.g. specifically binds a target DNA; e.g. is reasonably expected to transactivate genes involved in cell cycle arrest, such as p21; interact with the DNA repair and synthetic machinery, such as proliferating cellular nuclear antigen, GADD 45, or proteins modulating apoptosis. In a more preferred embodiment: the p63 protein regulates and/or modulates growth of an eukaryotic cell-cycle, e.g. a mammalian cell-cycle, e.g., a human cell-cycle; the p63 protein inhibits cell growth of a eukaryotic cell, e.g., a human cell; the p63 protein inhibits progression of a eukaryotic cell from G1 phase into S phase, e.g., inhibits progression of a mammalian cell from G1 phase into S phase, e.g., inhibits progression of a human cell from G1 phase into S phase; the tumor suppressor-protein suppresses tumor growth, e.g. in a tumor cell, e.g. in a tumor cell having an unimpaired p53 or *p63* or p53-like protein checkpoint. Thus, in one embodiment, the p-63 family of cell-regulatory proteins are involved in the modulation of cell growth or regulate the growth phenotype of a cell.

In yet other preferred embodiments, the recombinant tumor-suppressor-protein is a fusion protein further comprising a second polypeptide portion having an amino acid sequence from a protein unrelated the protein of SEQ ID Nos. 13-24. Such fusion proteins can be functional in a two-hybrid assay.

Another aspect of the present invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes a cell regulator-protein, or a fragment thereof, having an amino acid sequence at least 70% homologous to one of SEQ ID Nos. 13-24. In a more preferred embodiment: the nucleic acid encodes a protein having an amino acid sequence at least 80% homologous to SEQ ID No. 5, more preferably at least 90% homologous to SEQ ID No. 5, and most preferably at least 95% homologous to SEQ ID No. 5; the nucleic acid encodes a protein having an amino acid sequence at least 80% homologous to SEQ ID No. 8, more preferably at least 90% homologous to SEQ ID No. 8, and most preferably at least 95% homologous to SEQ ID No. 8 the nucleic acid encodes a protein having an amino acid sequence at least 80% homologous to SEQ ID No. 7, more preferably at least 90% homologous to SEQ ID No. 7, and most preferably at least 95% homologous to SEQ ID No. 7.

In a preferred embodiment: the subject cell regulator-protein specifically binds a target DNA or protein; for example transactivate genes involved in cell cycle arrest, such as p21; interact with the DNA repair and synthetic machinery, such as proliferating cellular nuclear antigen, GADD 45, or proteins modulating apoptosis. In a more preferred embodiment: the cell regulator-protein regulates and/or modulates growth of an eukaryotic cell-cycle, e.g. a mammalian cell-cycle, e.g., a human cell-cycle; the cell regulator-protein inhibits cell growth of a eukaryotic cell, e.g., a human cell; the cell regulator-protein inhibits progression of a eukaryotic cell from G1 phase into S phase, e.g., inhibits progression of a mammalian cell from G1 phase into S phase, e.g., inhibits progression of a human cell from G1 phase into S phase; the cell regulator-protein suppresses tumor growth, e.g. in a tumor cell, e.g. in a tumor cell having an unimpaired p53 or *p63* or p53-like protein checkpoint. Thus, in one embodiment, the p-63 family of cell-regulatory proteins are involved in the modulation of cell growth or regulate the growth phenotype of a cell.

In another embodiment, the nucleic acid hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of SEQ ID No. 1;

more preferably to at least 20 consecutive nucleotides of SEQ ID No. 1; more preferably to at least 40 consecutive nucleotides of SEQ ID No. 1.

In a further embodiment, the nucleic acid hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of SEQ ID No. 2; more preferably to at least 20 consecutive nucleotides of SEQ ID No. 2; more preferably to at least 40 consecutive nucleotides of SEQ ID No. 2.

In yet a further embodiment, the nucleic acid hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of SEQ ID No. 3; more preferably to at least 20 consecutive nucleotides of SEQ ID No. 3; more preferably to at least 40 consecutive nucleotides of SEQ ID No. 3.

In yet a further embodiment, the nucleic acid hybridizes under stringent conditions to a nucleic acid probe corresponding to at least 12 consecutive nucleotides of SEQ ID No. 6; more preferably to at least 20 consecutive nucleotides of SEQ ID No. 6; more preferably to at least 40 consecutive nucleotides of SEQ ID No. 6.

Furthermore, in certain embodiments, the cell regulator nucleic acid will comprise a transcriptional regulatory sequence, e.g. at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the cell regulator-gene sequence so as to render the recombinant cell regulator gene sequence suitable for use as an expression vector.

The present invention also features transgenic non-human animals, e.g. mice, which either express a heterologous cell regulator-gene, e.g. derived from humans, or which mis-express their own cell regulator-gene, e.g. where *p63*, p53 or p73 expression is disrupted. Such a transgenic animal can serve as an animal model for studying cellular disorders comprising mutated or mis-expressed cell regulator allelles.

The present invention also provides a probe/primer comprising a substantially purified oligonucleotide, wherein the oligonucleotide comprises a region of nucleotide sequence which hybridizes under stringent conditions to at least 10 consecutive nucleotides of sense or antisense sequence of one of SEQ ID Nos. 1-12, or naturally occurring mutants thereof. In preferred embodiments, the probe/primer further comprises a label group attached thereto and able to be detected, e.g. the label group is selected from a group consisting of radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors. Such

probes can be used as a part of a diagnostic test kit for identifying transformed cells, such as for measuring a level of a *p63*, p73 or p53 encoding nucleic acid in a sample of cells isolated from a patient; e.g. for measuring the mRNA level in a cell or determining whether the genomic cell regulator gene has been mutated or deleted.

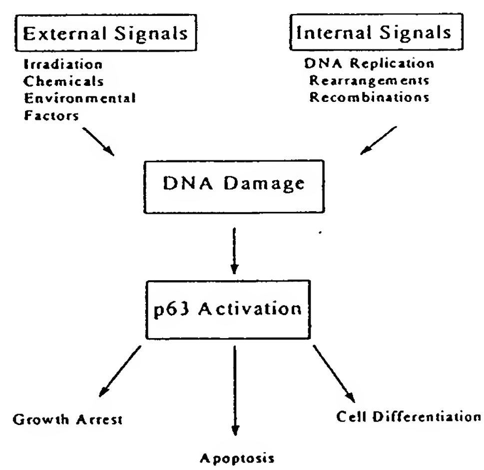
The present invention also provides a method for treating an animal having unwanted cell growth characterized by a loss of wild-type cell regulator-protein function, comprising administering a therapeutically effective amount of an agent able to transactivate genes involved in cell cycle arrest. For instance, a therapeutically effective amount of a p63 variant comprising a transactivating domain, for example Tap63γ. In one embodiment, the method comprises administering a nucleic acid construct encoding a cell regulator protein, e.g. a polypeptide represented in one of SEQ ID Nos. 13-24, under conditions wherein the construct is incorporated by cell regulator-deficient cells and the polypeptide is expressed, e.g. by gene therapy techniques. In another embodiment, the method comprises administering a cell regulator mimetic, e.g. a peptidomimetic, which binds to and transactivates genes involved in cell-cycle arrest.

Another aspect of the present invention provides a method of determining if a subject, e.g. a human patient, is at risk for a disorder characterized by unwanted cell proliferation, comprising detecting, in a tissue of the subject, the presence or absence of a genetic lesion characterized by at least one of (i) a mutation of a gene encoding a protein represented by one of SEQ ID Nos. 13-24, or a homolog thereof; or (ii) the mis-expression of the cell regulator-gene, e.g. the *p63*, p53 or p73 gene. In preferred embodiments: detecting the genetic lesion comprises ascertaining the existence of at least one of a deletion of one or more nucleotides from said gene, an addition of one or more nucleotides to said gene, an substitution of one or more nucleotides of said gene, a gross chromosomal rearrangement of said gene, a gross alteration in the level of a messenger RNA transcript of said gene, the presence of a non-wild type splicing pattern of a messenger RNA transcript of said gene, or a non-wild type level of said protein. For example, detecting the genetic lesion can comprise (i) providing a probe/primer comprising an oligonucleotide containing a region of nucleotide sequence which hybridizes to a sense or antisense sequence of one of SEQ ID Nos. 1-12, or naturally occurring mutants thereof, or 5' or 3' flanking sequences naturally associated with the cell regulator-gene; (ii) exposing the probe/primer to nucleic

acid of the tissue; and (iii) detecting, by hybridization of the probe/primer to the nucleic acid, the presence or absence of the genetic lesion; e.g. wherein detecting the lesion comprises utilizing the probe/primer to determine the nucleotide sequence of the cell regulator-gene and, optionally, of the flanking nucleic acid sequences; e.g. wherein detecting the lesion comprises utilizing the probe/primer in a polymerase chain reaction (PCR); e.g. wherein detecting the lesion comprises utilizing the probe/primer in a ligation chain reaction (LCR). In alternate embodiments, the level of said protein is detected in an immunoassay.

Yet another aspect of the invention pertains to a peptidomimetic which transactivates genes involved in cell-cycle arrest.

Like p53, *p63* is believed to be a multifunctional protein that exerts a variety of effects and plays a central role in the regulation of the cell cycle. For instance, over-expression of *p63*, particularly p63 variants comprising a transactivating domain may induce growth arrest, associated with the G_0/G_1 checkpoint, apoptosis occurring either through the G_0/G_1 checkpoint, or the S-phase or cell differentiation. In particular, *p63* is implicated in the mechanism that senses damaged DNA, and controls its repair and in the



induction of cell death. It is possible that, this may be accomplished by transactivation of the proliferating cell nuclear antigen (PCNA), involved in DNA replication and repair and the GADD-45 gene, whose product interacts with DNA. Furthermore, *p63* may also bind

several transcription associated proteins, which are involved in DNA damage and repair machinery. The role of *p63* in tumorigenesis may be demonstrated by using *p63* knocked out mice. Development of a high frequency of tumors in adult life would be indicative that *p63*, like p53, functions as a cell regulator gene. It is known in the art that p53 transactivates the pro-apoptotic gene, Bax (Miyashita and Reed 1995), in addition to an array of genes responsive to oxidative stress. Based on these observations p53 has been implicated in inducing cell-cycle arrest to allow for repair processes and/or the induction of cell death in the event of unmitigated stress. It was seen that p63 variants comprising a transactivation domain, i.e., TAp63γ, exhibited strong transcriptional activation of the p53 reporter. p63 variants lacking the transactivational domain, e.g., Δp63 are implicated in the regeneration of epithelial cells allowing proliferation of the epithelial cells. It is interesting that the ΔN variants, or dominant negative, versions of p63 seem to be the isotype expressed in many cancers. This may be tied to the observation that many types of cancer, particularly cervical carcinoma, show an overexpression of chromosome 3q, where the p63 gene is located. If this chromosomal amplification results in the overexpression of a ΔNp63 product which opposes p53 or transactivating p63 forms, the experiments that follow show that the dominant negative variants do in fact suppress the transactivating forms p63 and p53. Therefore, these p63 variants may be implicated in cancer biology and possible diagnostic/prognostic applications.

Thus, in one embodiment, the p-63 family of cell-regulatory proteins are involved in the modulation of cell growth or regulate the growth phenotype of a cell. Because of its various roles activation of *p63* may result in different outcomes as shown below:

Another aspect of the invention features related DNA and polypeptide sequences which are characterized by a particular percent homology or identity as determined by any of various mathematical algorithms known in the art. A number of mathematical algorithms have been developed to find and measure homology between two DNA or polypeptide sequences. For example the local homology algorithm of Smith and Waterman ((1981)Advances in Applied Mathematics 2:482-89) is used in the alignment software program called "BestFit," which is available from the GCG software package (Genetics Computer Group, 575 Science Drive, Madison, WI 53711; www.gcg.com). Other methods for aligning sequences include the homology alignment algorithm of Needleman and Wunsch ((1970) J. Mol. Biol. 48: 443) and the similarity search method of Pearson and Lipman ((1988) Proc. Natl. Acad. Sci. (USA) 85: 2444. These algorithms are available as computerized software such as GAP, FASTA and TFASTA in the Wisconsin Genetic Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI). Alternatively, sequences can be aligned manually by inspection, and the best analysis, yielding the greatest degree of homology, is chosen.

These methods to describe the sequence relationships between two or more polynucleotides require the analysis of certain elements of these sequences and the defining of certain parameters with which to analyze them. First, a "reference sequence" is a defined sequence used as a basis for a sequence comparison. A reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence is given in a sequence listing or may comprise a complete cDNA or gene sequence. Generally, a reference sequence is at least 25 nucleotides in length, frequently at least 25 nucleotides in length and often at least 50 nucleotides in length. Since two polynucleotides may each comprise both a sequence that is similar between the two polynucleotides and a sequence that is divergent between the two polynucleotides, sequence comparisons between two or more polynucleotides typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A comparison window, as used herein, refers to a conceptual segment of at least 20 contiguous nucleotide positions wherein a polynucleotide sequence may be compared to a reference sequence of at least 20 contiguous nucleotides and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions

or deletions (i.e. gaps) of 20 percent or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims. The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No. 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

3. Brief Description of the Figures

Figure 1. Primary Structure Alignments of *p53, p73,* and *p63*.
Human *p53*, human *p73β*, human Ta*p63γ* are presented, with residues identical to *p53* shaded in gray, and remaining consensus residues shaded in black.

Figure 2. Genomic Origin and Diversity of *p63* Isotypes

(A) Schematic of human *p63* gene structure highlighting positions of exons (coding sequences in black), the two promoters in exon one (black arrow) and exon 3' (gray arrow), and the major post-transcriptional splicing events which give rise to the major *p63* isotypes. **(B)** Domain structure of *p53*, *p73* α and β, and the major *p63* isotypes, Ta*p63* $\alpha\beta$, and γ, and ΔNp63 *a*, β, and *y*, highlighting regions involved in transactivation (TA), DNA binding, and oligomerization (oligo). White box denotes 39aa N-terminal extension unique to TA**p63*. Gray box represents 14aa unique to ΔN*p63*.

(C) Sequence alignment of N-termini of murine and human *p63* including that found in TA**p63*, TA*p63*, and ΔN*p63*.

(D) Alignment and comparison of the human *p63* *a*, β, and *y* C-terminal sequences.

Figure 3. Chromosomal Localization of Human and Mouse *p63* Gene.

(A) Schematic of chromosome 3 showing localization of human p63 gene at 3q27-29 based on fluorescence in situ hybridization with a p63 genomic PAC clone.

(B) Schematic of proximal end of mouse chromosome 16 showing location of murine p63 gene, as determined by linkage analysis against Jackson Laboratory interspecific backcross panels BBS and BSB. Loci mapping to similar positions are presented in alphabetical order, and missing typing inferred from surrounding data where assignment was unambiguous.

Figure 4. Immunolocalization of *p63* in Human Epithelial Tissues.

Paraffin sections of normal human epithelial tissues probed with monoclonal antibodies to *p63* using an alkaline phosphatase reporter system.

(A) *p63* staining in foreskin showing nuclear localization of *p63* in basal epithelial cells.

(B) *p63* localization to basal cells of ectocervical epithelium.

(C) *p63* localization in basal cells of vaginal epithelium.

(D) *p63* staining of basal cells of urothelium.

(E) *p63* staining of epithelial cell layer below luminal cells in prostate.

Figure 5. Tissue Distribution of *p63* Isotypes

(A) RT-PCR analysis of total RNA prepared from various adult mouse tissues using oligonucleotide primers designed to amplify TA*p63* isotypes, revealing a ~410pb product in heart, testis, kidney/adrenal, thymus, brain, and cerebellum.

(B) RT-PCR analysis using template RNA in (A) with oligonucleotide primers designed to yield a ~240bp product for ΔN*p63* isotypes, revealing expected product in kidney/adrenal, spleen, and thymus.

(C) Tel electrophoresis of RNA used as template in RT-PCR analyses to determine template integrity.

(D) Analysis of *p63* transcripts in human epithelial tissues. RT-PCR analyses of RNA from primary human foreskin keratinocytes, ectocervical cells, and the human cervical carcinoma cell line ME180 using oligonucleotides designed to amplify TA*p63* transcripts (left panel) and ΔN*p63* transcripts (right panel). The ME180 cells show products corresponding to both the TA*p63* and the ΔN*p63* transcripts, while RNA from primary keratinocytes and ectocervical cells yield predominantly products from ΔN*p63* transcripts.

(E) Western blot of primary human foreskin keratinocytes (1°HFK), ME180 human cervical carcinoma cells (ME180), and BHK cells expressing epitope-tagged p63 isotypes (TA**p63*γ, TA*p63*γ, ΔN*p63*γ, TA**p63a*, TA*p63a*, and ΔN*p63a*) using the 4A4 anti-*p63* monoclonal antibody. The major *p63* species in primary keratinocytes migrates slightly faster than the epitopetagged ΔN*p63a* protein.

Figure 6. Transactivation of *p53*-Reporter Genes by *p63* Isotypes

Transcriptional activation of *p53*-reporter gene in Saos-2 cells transfected with the indicated *p53* and *p63* expression constructs. Chemiluminescence signal from reporter β-galactosidase assays were performed and normalized for transfection efficiency using assays for co-transfected, constitutively expressed luciferase vectors. Error bars indicate standard deviation in triplicate assays.

Figure 7. Induction of Apoptosis by *p63* Isotypes

BHK cells transfected with idential amounts of wildtype *p53* **(A)** mutant *p53* **(B)**, TA*p63*γ (C), ΔN*p63*γ**(D)**, and ΔN*p63a*(E), were processed for immunofluorescence after 16 hours using epitope-tagged antibodies (left panel) and Hoechst dye for DNA staining (right panel).

Wildtype *p53*- and TA*p63*γ-expressing cells showed high levels of apoptosis (arrows) despite very low protein expression, while ΔN*p63*γ yielded high protein expression and modest levels of apoptosis. Mutant *p53* and ΔN*p63*a showed high levels of protein expression but control levels of apoptosis.

Figure 8. Interactions Amongst *p63* Isotypes and *p53* in Transactivation Assays
(A) Transactivation analysis in Saos-2 cells transfected with a constant amount of wildtype *p53* expression vector, minimal *p53*-reporter construct, and either ΔN*p63*γ or ΔN*p63a* expression vectors at ratios of 1:5 or 1:1 with respect to *p53*, as indicated.
(B) Transactivation analysis in Saos-2 cells transfected with a constant amount of TA*p63*γ expression vector, *p53*-reporter construct, and either ΔN*p63*γ or ΔN*p63*a expression vectors at ratios of 1:5 or 1:1 with respect to TA*p63*γ, as indicated.

Figure 9. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 1 and 13 respectively.

Figure 10. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 2 and 14 respectively.

Figure 11. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 3 and 15 respectively.

Figure 12. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 4 and 16 respectively.

Figure 13. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 5 and 17 respectively.

Figure 14. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 6 and 18 respectively.

Figure 15. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 7 and 19 respectively.

Figure 16. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 8 and 20 respectively.

Figure 17. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 9 and 21 respectively.

Figure 18. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 10 and 22 respectively.

Figure 19. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 11 and 23 respectively.

Figure 20. Represents nucleic acid and amino acid sequences represented by SEQ ID Nos.: 12 and 24 respectively.

Figure 21 shows induction of transactivating version of p63 upon UV irradiation. The time course is similar, but not identical, to p53's induction by UV. This is the first demonstration that p63 (and in particular, the transactivating, p53-like, version) can respond to stress signals such as UV/DNA damage.

Figure 22 shows that p63 protein levels, while high in the basal, proliferative/regenerative layer of squamous epithelia, decreases dramatically upon differentiation/maturation of these keratinocytes. This may implicate p63 in differntiation processes that are important for both oncogenesis and normal development.

Figure 23 shows p63 RNA expression in some human cancer cell lines, mostly cervical carcinoma.

Figure 24 just shows p63 RNA expression in some human breast cancer cell lines. It is useful to note that p63 is expressed in these cancers. ΔN versions also strongly expresses in some of these lines.

Figure 25. Shows the results of an electrophoretic shift assay.

4. Detailed Description of the Invention

4.1. General

The present invention concerns the discovery of a new family of cell regulatory proteins, referred to herein as the *p63* family of proteins, which demonstrate certain sequence identity to known tumor suppressor proteins p53 and p73. The *p63* proteins may generally be represented by the general formula: X-Y-Z, wherein X represents the N-termini of the proteins, e.g. a ΔN, a TA*, or TA polypeptide sequence *(infra)*, Y represents the core domain of the protein, and Z represents the C termini, e.g., the α, β, or γ polypeptide sequences (*infra*). The mouse and human *p63* were identified by using a novel PCR based strategy. Specifically, it was observed that the intron-exon organization was conserved between p53 and p73, by using the known exon and intron sizes for these genes it was possible to amplify portions of two adjacent exons and the intervening intron. The rationale being that sequence similarities between the exonic regions would demonstrate a related gene, while differences in size would indicate a novel family member. By this technique we identified at least one new paralog of the p53/p73/*p63* related family. Mouse cDNA was isolated using the RACE (5' rapid amplification of cDNA ends) technique and the sequencing of the amplification product indicated that the amplified cDNA possessed a truncated N-terminus, i.e. the transactivation domain was absent in this product. Additional splice variants of the mouse *p63* were identified by screening a cDNA library with a probe corresponding to exons 5 through 9 of *p63*. In general, splice variants differing in the C-terminus have been designated as α , β, and γ forms, whereas *p63* members differing in the N-terminus are designated as the ΔN and TA forms, wherein the ΔN form lack the transactivational domain.

The appended sequence listing, provides a list of the nucleic acid and protein sequences that are included within the scope of this invention.

Table 1
Guide to *p63* sequences in Sequence Listing

	Nucleotide Sequence	Amino Acid Sequence
hu-TA*p63*α	SEQ ID No. 1	SEQ ID No. 13
hu-TA*p63*β	SEQ ID No. 2	SEQ ID No. 14
hu-TA*p63*γ	SEQ ID NO. 3	SEQ ID NO. 15
hu-ΔN*p63*α	SEQ ID No. 4	SEQ ID No. 16
hu-ΔN*p63*β	SEQ ID No. 5	SEQ ID No. 17
hu-ΔN*p63*γ	SEQ ID No. 6	SEQ ID No. 18
mu-TA**p63*α	SEQ ID No. 7	SEQ ID No. 19
mu-TA**p63*β	SEQ ID No. 8	SEQ ID No. 20
mu-TA**p63*γ	SEQ ID No. 9	SEQ ID No.21
mu-ΔN*p63*α	SEQ ID No. 10	SEQ ID No. 22
mu-ΔN*p63*β	SEQ ID No. 11	SEQ ID No. 23
mu-ΔN*p63*γ	SEQ ID No. 12	SEQ ID No.24

By fluorescence *in situ* hybridization (FISH), the human *p63* gene has been localized to chromosomal position 3q27-29. Early expression data suggests that *p63* is expressed at steady-state detectable levels in various adult tissues. The p63 proteins can be divided into two classes - one with *p53*-like properties and the other lacking *p53*-associated functions such as transcriptional activation and apoptosis. *p63* transcripts were detected in a wide range of adult tissues, including heart, testis, kidney/adrenal, spleen, thymus, and brain, typically showing a predominance of either the TA or ΔN isotypes. Analysis of human epithelial tissues has provided further insights into endogenous *p63* expression, as immunohistochemistry with anti-*p63* monoclonal antibodies revealed strong and discrete labeling of the nuclei of basal cells within the epidermis, ectocervical epithelium, urothelium, and prostate epithelium, while more differentiated, suprabasal cells showed little or no labeling. The presence of *p63* in basal cell layers of epithelial tissues is significant because these cells have an essential role in the regenerative processes of these epithelia. Specifically, the basal cells are thought to be progenitor, or stem, populations for

suprabasal layers, and as such are the proliferative components of these tissues. This finding that these epithelial cells predominantly express ΔN*p63* isotypes is consistent with growth-permitting requirements of proliferating cells, and may underlie the regenerative abilities of normal epithelial tissues.

It is contemplated by the present invention that the cloned *p63*- genes set out in the appended sequence listing, in addition to representing a inter-species family of related genes, are also each part of an intra-species family. That is, it is anticipated that other paralogs of the human and mouse *p63* proteins exist in those animals, and orthologs of each *p63* gene are conserved amongst other animals. For instance, at low to medium stringency conditions, another transcript was observed and this probably represents a new paralogous gene related to the p/53/p73/*p63* family of genes, or may a splice variant of *p63* as set forth in SEQ ID No. 1.

The p53 protein consists of 393 amino acids with various functional domains, evolutionarily conserved domains and regions which have been designated as mutational hotspots. The functional domains include: a transactivational domain (amino acids 20-50), sequence specific DNA binding domain (amino acids 100-293) nuclear localization sequence (amino acids 316-325), and the oligomerization domain (amino acids 319-360). It was found that the homology between p73 and p53 was considerable within the most conserved p53 domains. The transactivational domain (amino acids 1-45) exhibited 29% identity, the DNA binding region 63 % identity (amino acids 113-290) and the oligomerization domain 38 % identity with p53 (amino acids 319-363).

Interestingly it was observed that the sequence identity between the mouse and human *p63* sequences was considerably high, both at the nucleotide and protein levels, specifically, the mouse and human *p63* beta forms exhibit 90.8% identity at the DNA level and 98.6% identity at the protein level, the alpha forms showed 83.4 % at the DNA level and 97.8% at the protein level. The sequence identity between *p63* and p73 alpha form is about 57.4% identity and the *p63* and p73 beta form shows about 69.7% identity at the protein level. *p63* alpha form and p53 exhibit 43.8% identity at the protein level.

Accordingly, certain aspects of the present invention relate to nucleic acids encoding *p63* polypeptides, the *p63* polypeptides themselves (including various fragments), antibodies immunoreactive with *p63* proteins, and preparations of such compositions.

Moreover, the present invention provides diagnostic and therapeutic assays and reagents for detecting and treating disorders involving, for example, aberrant expression (or loss) of *p63*.

In addition, drug discovery assays are provided for identifying agents which can modulate the biological function of *p63* proteins, such as by altering the binding of *p63* molecules to target proteins or DNA sequences, or other extracellular/matrix factors. Furthermore, based on the considerable sequence identity with p53, the skilled artisan could reasonably appreciate that the *p63*-family of proteins would play a significant role as a cell regulator, a tumor suppressor, function in cell cycle control various developmental processes, apoptosis, gene expression and tumorigenesis. *p63* may also be implicated in hematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation (and degenerative disorders related thereto). It is known that p53 probably exists as a tetramer and dominant negative mutants of p53, which function by overwhelming the wild-type protein and prevent it from functioning probably forms a heteromeric protein containing both the mutant and wild-type subunits in which the wild type subunits are unable to function. In one aspect, the inventors demonstrate that the *p63* protein products lacking the transactivational domains, for example the ΔN*p63*α and ΔN*p63*γ have dominant negative effects on the activity of p53. . Similarly, these dominant negative forms may exert their function by forming a heteromeric protein with either wild-type p53 or *p63* and hence prevent the wild type protein from functioning.

4.2. <u>Definitions</u>

For convenience, the meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below.

A "*p63*" cell regulatory protein as referred to herein, refers to proteins that may generally be represented by the formula: X-Y-Z, wherein X represents the N-termini of the proteins, e.g. a TA, TA*, or ΔN polypeptide sequence, Y represents the core domain of the protein, and Z represents the C termini, e.g., the α, β, or γ polypeptide sequences. Illustrative examples include proteins represented by SEQ ID Nos. 13-24, and homologs thereof.

A "p53 protein" refers to the sequence designated by GenBank Accession Number K03199 and orthologs thereto.

"P73" refers to the sequences disclosed by Kaghad *et al.*, Cell 90:809-819 (1997).

The term "agonist", as used herein, is meant to refer to an agent that mimics or upregulates (e.g. potentiates or supplements) *p63* bioactivity. A *p63* agonist can be a wild-type *p63* protein or derivative thereof having at least one bioactivity of the wild-type *p63*. A *p63* agonist can also be a compound that upregulates expression of a gene or which increases at least one bioactivity of a *p63* protein. An agonist can also be a compound which increases the interaction of a *p63* polypeptide with another molecule, e.g, a target peptide or nucleic acid.

"Antagonist" as used herein is meant to refer to an agent that downregulates (e.g. suppresses or inhibits) at least one *p63* bioactivity. A *p63* antagonist can be a compound which inhibits or decreases the interaction between a *p63* protein and another molecule, e.g., a target peptide, such as angiotensin I or a kinin. Accordingly, a preferred antagonist is a compound which inhibits or decreases hydrolysis of a target peptide. An antagonist can also be a compound that downregulates expression of a *p63* gene or which reduces the amount of *p63* protein present.

The term "antibody" as used herein is intended to whole antibodies, e.g., of any isotype (IgG, IgA, IgM, IgE, etc), and includes fragments thereof which are also specifically reactive with an vertebrate, e.g., mammalian, *p63* protein. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. Thus, the term includes segments of proteolytically-cleaved or recombinantly-prepared portions of an antibody molecule that are capable of selectively reacting with a *p63* protein. Nonlimiting examples of such proteolytic and/or recombinant fragments include Fab, F(ab')2, Fab' , Fv, fragments, and single chain antibodies (scFv) containing a V[L] and/or V[H] domain joined by a peptide linker. The scFv's may be covalently or non-covalently linked to form antibodies having two or more binding sites. The subject invention includes polyclonal, monoclonal, or other purified preparations of antibodies and recombinant antibodies.

The term "allele", which is used interchangeably herein with "allelic variant" refers to alternative forms of a gene or portions thereof. Alleles occupy the same locus or position

on homologous chromosomes. When a subject has two identical alleles of a gene, the subject is said to be homozygous for that gene or allele. When a subject has two different alleles of a gene, the subject is said to be heterozygous for the gene. Alleles of a specific gene can differ from each other in a single nucleotide, or several nucleotides, and can include substitutions, deletions, and/or insertions of nucleotides. An allele of a gene can also be a form of a gene containing mutations.

The term "allelic variant of a polymorphic region of an *p63* gene" refers to a region of the *p63* gene having one of several nucleotide sequences found in that region of the gene in other individuals.

The phenomenon of "apoptosis" is well known, and can be described as a programmed death of cells. As is known, apoptosis is contrasted with "necrosis", a phenomenon when cells die as a result of being killed by a toxic material, or other external effect. Apoptosis involves chromatic condensation, membrane blebbing, and fragmentation of DNA, all of which are generally visible upon microscopic examination.

"Biological activity" or "bioactivity" or "activity" or "biological function", which are used interchangeably, for the purposes herein means an effector or antigenic function that is directly or indirectly performed by a *p63* polypeptide (whether in its native or denatured conformation), or by any subsequence thereof. Biological activities include binding to polypeptides, particularly in the formation of homomeric complexes or heteromeric complexes with other p53 or p73 homologs, binding to other proteins or molecules; activity as a DNA binding protein, as a transcription regulator, ability to bind damaged DNA etc. A *p63* bioactivity can be modulated by directly affecting the *p63* polypeptide. Alternatively, an *p63* bioactivity can be altered by modulating the level of the *p63* polypeptide, such as by modulating expression of the *p63* gene.

As used herein the term "bioactive fragment of a *p63* polypeptide" refers to a fragment of a full-length *p63* polypeptide, wherein the fragment specifically agonizes (mimics) or antagonizes (inhibits) the activity of a wild-type *p63* polypeptide. The bioactive fragment preferably is a fragment capable of interacting with at least one other molecule, protein or DNA, with which a full length *p63* protein can bind.

The term "an aberrant activity", as applied to an activity of a polypeptide such as *p63*, refers to an activity which differs from the activity of the wild-type or native polypeptide or which differs from the activity of the polypeptide present in a healthy subject. An activity of a polypeptide can be aberrant because it is stronger than the activity

of its native counterpart. Alternatively, an activity can be aberrant because it is weaker or absent relative to the activity of its native counterpart. An aberrant activity can also be a change in the activity; for example, an aberrant polypeptide can interact with a different target peptide. A cell can have an aberrant *p63* activity due to overexpression or underexpression of the gene encoding *p63*.

"Cells," "host cells" or "recombinant host cells" are terms used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A "chimeric polypeptide" or "fusion polypeptide" is a fusion of a first amino acid sequence encoding one of the subject *p63* polypeptides with a second amino acid sequence defining a domain (e.g. polypeptide portion) foreign to and not substantially homologous with any domain of a *p63* polypeptide. A chimeric polypeptide may present a foreign domain which is found (albeit in a different polypeptide) in an organism which also expresses the first polypeptide, or it may be an "interspecies", "intergenic", etc. fusion of polypeptide structures expressed by different kinds of organisms. In general, a fusion polypeptide can be represented by the general formula $(X)_n$-$(Y)_m$-$(Z)_n$, wherein Y represents a portion of the *p63* polypeptide, and X and Z are each independently absent or represent amino acid sequences which are not related to the native *p63* sequence found in an organism, or which are not found asa polypeptide chain contigous with the *p63* sequence, where m is an integer greater than or equal to one, and each occurence of n is, indepenedently, 0 or an integer greater than or equal to 1 (n and m are preferably no greater than 5 or 10).

The term “nucleotide sequence complementary to the nucleotide sequence set forth in SEQ ID NO. x” refers to the nucleotide sequence of the complementary strand of a nucleic acid strand having SEQ ID NO. x. The term “complementary strand” is used herein interchangeably with the term “complement”. The complement of a nucleic acid strand can be the complement of a coding strand or the complement of a non-coding strand.

A "delivery complex" shall mean a targeting means (e.g. a molecule that results in higher affinity binding of a gene, protein, polypeptide or peptide to a target cell surface and/or increased cellular or nuclear uptake by a target cell). Examples of targeting means include: sterols (e.g. cholesterol), lipids (e.g. a cationic lipid, virosome or liposome), viruses

(e.g. adenovirus, adeno-associated virus, and retrovirus) or target cell specific binding agents (e.g. ligands recognized by target cell specific receptors). Preferred complexes are sufficiently stable *in vivo* to prevent significant uncoupling prior to internalization by the target cell. However, the complex is cleavable under appropriate conditions within the cell so that the gene, protein, polypeptide or peptide is released in a functional form.

As is well known, genes or a particular polypeptide may exist in single or multiple copies within the genome of an individual. Such duplicate genes may be identical or may have certain modifications, including nucleotide substitutions, additions or deletions, which all still code for polypeptides having substantially the same activity. The term "DNA sequence encoding a *p63* polypeptide" may thus refer to one or more genes within a particular individual. Moreover, certain differences in nucleotide sequences may exist between individual organisms, which are called alleles. Such allelic differences may or may not result in differences in amino acid sequence of the encoded polypeptide yet still encode a polypeptide with the same biological activity.

A disease, disorder or condition "associated with" or "characterized by" an aberrant *p63* activity refers to a disease, disorder or condition in a subject which is caused by or contributed to by an aberrant *p63* activity.

The term "equivalent" is understood to include nucleotide sequences encoding functionally equivalent *p63* polypeptides or functionally equivalent peptides having an activity of an *p63* protein such as described herein. Equivalent nucleotide sequences will include sequences that differ by one or more nucleotide substitutions, additions or deletions, such as allelic variants; and will, therefore, include sequences that differ from the nucleotide sequence of the *p63* gene shown in SEQ ID NOs: 1-12, due to the degeneracy of the genetic code.

As used herein, the terms "gene", "recombinant gene" and "gene construct" refer to a nucleic acid comprising an open reading frame encoding a *p63* polypeptide of the present invention, including both exon and (optionally) intron sequences.

A "recombinant gene" refers to nucleic acid encoding a *p63* polypeptide and comprising *p63*-encoding exon sequences, though it may optionally include intron sequences which are derived from, for example, a chromosomal *p63* gene or from an unrelated chromosomal gene. Exemplary recombinant genes encoding the subject *p63* polypeptide are represented in the appended Sequence Listing. The term "intron" refers to a DNA sequence present in a given *p63*-gene which is not translated into protein and is generally found between exons.

The term “growth" or “growth state" of a cell refers to the proliferative state of a cell as well as to its differentiative state. Accordingly, the term refers to the phase of the cell cycle in which the cell is, e.g., G0, G1, G2, prophase, metaphase, or telophase, as well as to its state of differentiation, e.g., undifferetiated, partially differentiated, or fully differentiated. Without wanting to be limited, differentiation of a cell is usually accompanied by a decrease in the proliferative rate of a cell.

"Homology" or "identity" or "similarity" refers to sequence similarity between two peptides or between two nucleic acid molecules, with identity being a more strict comparison. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When a position in the compared sequence is occupied by the same base or amino acid, then the molecules are identical at that position. A degree of homology or similarity or identity between nucleic acid sequences is a function of the number of identical or matching nucleotides at positions shared by the nucleic acid sequences. A degree of identity of amino acid sequences is a function of the number of identical amino acids at positions shared by the amino acid sequences. A degree of homology or similarity of amino acid sequences is a function of the number of amino acids, i.e. structurally related, at positions shared by the amino acid sequences. An "unrelated" or "non-homologous" sequence shares less than 40 % identity, though preferably less than 25 % identity, with one of the *p63* sequences of the present invention.

The term "interact" as used herein is meant to include detectable interactions (e.g. biochemical interactions) between molecules, such as interaction between protein-protein, protein-nucleic acid, nucleic acid-nucleic acid, and protein-small molecule or nucleic acid-small molecule in nature.

The term "isolated" as used herein with respect to nucleic acids, such as DNA or RNA, refers to molecules separated from other DNAs, or RNAs, respectively, that are present in the natural source of the macromolecule. For example, an isolated nucleic acid encoding one of the subject *p63* polypeptides preferably includes no more than 10 kilobases (kb) of nucleic acid sequence which naturally immediately flanks the *p63* gene in genomic DNA, more preferably no more than 5kb of such naturally occurring flanking sequences, and most preferably less than 1.5kb of such naturally occurring flanking sequence. The term isolated as used herein also refers to a nucleic acid or peptide that is substantially free

of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides.

The term "modulation" as used herein refers to both upregulation (i.e., activation or stimulation (e.g., by agonizing or potentiating)) and downregulation (i.e. inhibition or suppression (e.g., by antagonizing, decreasing or inhibiting)).

The term “mutated gene" refers to an allelic form of a gene, which is capable of altering the phenotype of a subject having the mutated gene relative to a subject which does not have the mutated gene. If a subject must be homozygous for this mutation to have an altered phenotype, the mutation is said to be recessive. If one copy of the mutated gene is sufficient to alter the genotype of the subject, the mutation is said to be dominant. If a subject has one copy of the mutated gene and has a phenotype that is intermediate between that of a homozygous and that of a heterozygous subject (for that gene) , the mutation is said to be co-dominant.

The "non-human animals" of the invention include mammalians such as rodents, non-human primates, sheep, dog, cow, chickens, amphibians, reptiles, etc. Preferred non-human animals are selected from the rodent family including rat and mouse, most preferably mouse, though transgenic amphibians, such as members of the *Xenopus* genus, and transgenic chickens can also provide important tools for understanding and identifying agents which can affect, for example, embryogenesis and tissue formation. The term "chimeric animal" is used herein to refer to animals in which the recombinant gene is found, or in which the recombinant gene is expressed in some but not all cells of the animal. The term "tissue-specific chimeric animal" indicates that one of the recombinant *p63* gene sis present and/or expressed or disrupted in some tissues but not others.

As used herein, the term "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). The term should also be understood to include, as equivalents, analogs of either RNA or DNA made from nucleotide analogs, and, as applicable to the embodiment being described, single (sense or antisense) and double-stranded polynucleotides.

The term “polymorphism" refers to the coexistence of more than one form of a gene or portion (e.g., allelic variant) thereof. A portion of a gene of which there are at least two

different forms, i.e., two different nucleotide sequences, is referred to as a "polymorphic region of a gene". A polymorphic region can be a single nucleotide, the identity of which differs in different alleles. A polymorphic region can also be several nucleotides long.

A "polymorphic gene" refers to a gene having at least one polymorphic region.

As used herein, the term "promoter" means a DNA sequence that regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in cells. The term encompasses "tissue specific" promoters, i.e. promoters, which effect expression of the selected DNA sequence only in specific cells (e.g. cells of a specific tissue). The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well. The term also encompasses non-tissue specific promoters and promoters that constitutively express or that are inducible (i.e. expression levels can be controlled).

The terms "protein", "polypeptide" and "peptide" are used interchangeably herein when referring to a gene product.

The term "recombinant protein" refers to a polypeptide of the present invention which is produced by recombinant DNA techniques, wherein generally, DNA encoding a *p63* polypeptide is inserted into a suitable expression vector which is in turn used to transform a host cell to produce the heterologous protein. Moreover, the phrase "derived from", with respect to a recombinant *p63* gene, is meant to include within the meaning of "recombinant protein" those proteins having an amino acid sequence of a native *p63* polypeptide, or an amino acid sequence similar thereto which is generated by mutations including substitutions and deletions (including truncation) of a naturally occurring form of the polypeptide.

"Small molecule" as used herein, is meant to refer to a composition, which has a molecular weight of less than about 5 kD and most preferably less than about 4 kD. Small molecules can be nucleic acids, peptides, polypeptides, peptidomimetics, carbohydrates, lipids or other organic (carbon containing) or inorganic molecules. Many pharmaceutical companies have extensive libraries of chemical and/or biological mixtures, often fungal, bacterial, or algal extracts, which can be screened with any of the assays of the invention to identify compounds that modulate a *p63* bioactivity.

As used herein, the term "specifically hybridizes" or "specifically detects" refers to the ability of a nucleic acid molecule of the invention to hybridize to at least approximately 6, 12, 15, 20, 30, 50, 100, 150, 200, 300, 350, 400 or 425 contigous nucleotides of a *p63*

gene, such as designated in any one of SEQ ID Nos: 1-12, or a sequence complementary thereto, or naturally occuring mutants thereof, such that it has less than 15%, preferably less than 10%, and more preferably less than 5% background hybridization to a cellular nucleic acid (e.g. mRNA or genomic DNA) encoding a protein other than a *p63* protein, as defined herein. In preferred embodiments, the oligonucleotide probe detects only a *p63* gene, e.g., it does not substantially hybridize to transcripts encoding either p53 or p73, or complements thereof.

"Transcriptional regulatory sequence" is a generic term used throughout the specification to refer to DNA sequences, such as initiation signals, enhancers, and promoters, which induce or control transcription of protein coding sequences with which they are operably linked. In preferred embodiments, transcription of one of the *p63* genes is under the control of a promoter sequence (or other transcriptional regulatory sequence) which controls the expression of the recombinant gene in a cell-type in which expression is intended. It will also be understood that the recombinant gene can be under the control of transcriptional regulatory sequences which are the same or which are different from those sequences which control transcription of the naturally-occurring forms of *p63* polypeptide.

As used herein, the term "transfection" means the introduction of a nucleic acid, e.g., via an expression vector, into a recipient cell by nucleic acid-mediated gene transfer. "Transformation", as used herein, refers to a process in which a cell's genotype is changed as a result of the cellular uptake of exogenous DNA or RNA, and, for example, the transformed cell expresses a recombinant form of a *p63* polypeptide or, in the case of anti-sense expression from the transferred gene, the expression of a naturally-occurring form of the *p63* polypeptide is disrupted.

As used herein, the term "transgene" means a nucleic acid sequence (encoding, e.g., one of the *p63* polypeptides, or an antisense transcript thereto) which has been introduced into a cell. A transgene could be partly or entirely heterologous, i.e., foreign, to the transgenic animal or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (e.g., it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can also be present in a cell in the form of an episome. A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, such as introns, that may be necessary for optimal expression of a selected nucleic acid.

A "transgenic animal" refers to any animal, preferably a non-human mammal, bird or an amphibian, in which one or more of the cells of the animal contain heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or *in vitro* fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of the *p63* polypeptide, e.g. either agonistic or antagonistic forms. However, transgenic animals in which the recombinant *p63* gene is silent are also contemplated, as for example, the FLP or CRE recombinase dependent constructs described below. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more *p63* genes is caused by human intervention, including both recombination and antisense techniques.

The term "treating" as used herein is intended to encompass curing as well as ameliorating at least one symptom of the condition or disease.

The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of preferred vector is an episome, i.e., a nucleic acid capable of extra-chromosomal replication. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. Vectors capable of directing the expression of genes to which they are operatively linked are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of "plasmids" which refer generally to circular double stranded DNA loops which, in their vector form are not bound to the chromosome. In the present specification, "plasmid" and "vector" are used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors which serve equivalent functions and which become known in the art subsequently hereto.

The term "wild-type allele" refers to an allele of a gene which, when present in two copies in a subject results in a wild-type phenotype. There can be several different wild-type alleles of a specific gene, since certain nucleotide changes in a gene may not affect the phenotype of a subject having two copies of the gene with the nucleotide changes.

4.3. Nucleic Acids of the Present Invention

As described below, one aspect of the invention pertains to isolated nucleic acids comprising a nucleotide sequence encoding *p63* polypeptides, variants and/or equivalents of such nucleic acids.

Preferred nucleic acids including coding sequences from vertebrate *p63* gene, especially a mammalian *p63* gene. Regardless of the species, particularly preferred *p63* nucleic acids encode polypeptides that are at least 70%, 75%, 80%, 90%, 95%, 97%, or 98% similar to an amino acid sequence of a vertebrate *p63* protein. In one embodiment, the nucleic acid is a cDNA encoding a polypeptide having at least one bio-activity of the subject *p63* polypeptide. Preferably, the nucleic acid includes all or a portion of the nucleotide sequence corresponding to the nucleic acid of SEQ ID Nos 1-12.

Still other preferred nucleic acids of the present invention encode a *p63* polypeptide which is comprised of at least 2, 5, 10, 25, 50, 100, 150 or 200 contiguous amino acid residues. For example, preferred nucleic acid molecules for use as probes/primer or antisense molecules (i.e. noncoding nucleic acid molecules) can comprise at least about 6, 12, 20, 30, 50, 60, 70, 80, 90 or 100 base pairs in length, whereas coding nucleic acid molecules can comprise about 50, 60, 70, 80, 90, or 100 base pairs.

In yet another embodiment, the fragment includes the DNA binding domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

Another aspect of the invention provides a nucleic acid which hybridizes under low, medium, or high stringency conditions to a nucleic acid sequences represented by SEQ ID NOs: 1, 2, 3, or 4. Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-12.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or temperature of salt concentration may be held constant while the

other variable is changed. In a preferred embodiment, a *p63* nucleic acid of the present invention will bind to one of SEQ ID NOs 1-12 under moderately stringent conditions, for example at about 2.0 x SSC and about 40°C. In a particularly preferred embodiment, a *p63* nucleic acid of the present invention will bind to one of SEQ ID NOs: 1-12 under high stringency conditions.

Preferred nucleic acids have a sequence at least 70%, and more preferably 80% identical and more preferably 90% and even more preferably at least 95% identical to an amino acid sequence of a *p63* gene, e.g., such as a sequence shown in one of SEQ ID NOS: 13-24. Nucleic acids at least 90%, more preferably 95%, and most preferably at least about 98-99% identical with a nucleic sequence represented in one of SEQ ID NOS: 1-12 are of course also within the scope of the invention. In preferred embodiments, the nucleic acid is mammalian and in particularly preferred embodiments, includes all or a portion of the nucleotide sequence corresponding to the coding region of one of SEQ ID NOs: 1-12.

Nucleic acids having a sequence that differs from the nucleotide sequences shown in one of SEQ ID NOs: 1-12 due to degeneracy in the genetic code are also within the scope of the invention. Such nucleic acids encode functionally equivalent peptides (i.e., a peptide having a biological activity of a *p63* polypeptide) but differ in sequence from the sequence shown in the sequence listing due to degeneracy in the genetic code. For example, a number of amino acids are designated by more than one triplet. Codons that specify the same amino acid, or synonyms (for example, CAU and CAC each encode histidine) may result in "silent" mutations which do not affect the amino acid sequence of a *p63* polypeptide. However, it is expected that DNA sequence polymorphisms that do lead to changes in the amino acid sequences of the subject *p63* polypeptides will exist among mammals. One skilled in the art will appreciate that these variations in one or more nucleotides (e.g., up to about 3-5% of the nucleotides) of the nucleic acids encoding polypeptides having an activity of a *p63* polypeptide may exist among individuals of a given species due to natural allelic variation.

Also within the scope of the invention are nucleic acids encoding splicing variants of *p63* proteins or natural homologs of *p63* proteins which consist essentially of one of the two units of *p63*. Such homologs can be cloned by hybridization or PCR, as further described herein.

The polynucleotide sequence may also encode for a leader sequence, e.g., the natural leader sequence or a heterologous leader sequence. For example, the desired DNA sequence may be fused in the same reading frame to a DNA sequence which aids in expression and

secretion of the polypeptide from the host cell, for example, a leader sequence which functions as a secretory sequence for controlling transport of the polypeptide from the cell. The protein having a leader sequence is a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the protein.

The polynucleotide of the present invention may also be fused in frame to a marker sequence, also referred to herein as "Tag sequence" encoding a "Tag peptide", which allows for marking and/or purification of the polypeptide of the present invention. In a preferred embodiment, the marker sequence is a hexahistidine tag, e.g., supplied by a PQE-9 vector. Numerous other Tag peptides are available commercially. Other frequently used Tags include myc-epitopes (e.g., see Ellison et al. (1991) *J Biol Chem 266*:21150-21157) which includes a 10-residue sequence from c-myc, the pFLAG system (International Biotechnologies, Inc.), the pEZZ-protein A system (Pharmacia, NJ), and a 16 amino acid portion of the *Haemophilus influenza* hemagglutinin protein. Furthermore, any polypeptide can be used as a Tag so long as a reagent, e.g., an antibody interacting specifically with the Tag polypeptide is available or can be prepared or identified.

As indicated by the examples set out below, *p63* protein-encoding nucleic acids can be obtained from mRNA present in any of a number of eukaryotic cells, e.g., and is preferably obtained from metazoan cells, more preferably from vertebrate cells and even more preferably from mammalian cells. It should also be possible to obtain nucleic acids encoding *p63* polypeptides of the present invention from genomic DNA from both adults and embryos. For example, a gene encoding a *p63* protein can be cloned from either a cDNA or a genomic library in accordance with protocols described herein, as well as those generally known to persons skilled in the art. cDNA encoding a *p63* protein can be obtained by isolating total mRNA from a cell, e.g., a vertebrate cell, a mammalian cell, or a human cell, including embryonic cells. Double stranded cDNAs can then be prepared from the total mRNA, and subsequently inserted into a suitable plasmid or bacteriophage vector using any one of a number of known techniques. The gene encoding a *p63* protein can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. A preferred nucleic acid is a cDNA represented by a sequence selected from the group consisting of SEQ ID NOs: 1-12.

Preferred nucleic acids encode a vertebrate *p63* polypeptide comprising an amino acid sequence at least 80% identical, more preferably 90% identical and most preferably 95% identical with an amino acid sequence contained in any of SEQ ID Nos: 13-24. Nucleic acids which encode polypeptides at least about 90%, more preferably at least about 95%,

and most preferably at least about 98-99% homology with an amino acid sequence represented in SEQ ID No: 13-24 are also within the scope of the invention. In one embodiment, the nucleic acid is a cDNA encoding a peptide having at least one activity of the subject vertebrate *p63* polypeptide. Preferably, the nucleic acid includes all or a portion of the nucleotide sequence corresponding to the coding region of SEQ ID Nos: 1-12.

Preferred nucleic acids encode a bioactive fragment of a vertebrate *p63* polypeptide comprising an amino acid sequence at least 80% identical or identical, more preferably 90% identical or identical and most preferably 95% identical or identical with an amino acid sequence selected from the group consisting of SEQ ID No: 13-24. For instance, these bioactive fragments may include the DNA binding domains, transactivation domains, oligomerization domain, etc. Nucleic acids which encode polypeptides which are at least about 90%, more preferably at least about 95%, and most preferably these at least about 98-99% homologous or identical, with an amino acid sequence represented in SEQ ID No: 13-24 are also within the scope of the invention.

Preferred bioactive fragments of *p63* polypeptides include polypeptides having one or more of the following biological activities: activity as a tumor suppressor, functions in cell cycle control of various developmental processes, apoptosis, gene expression, modulation of proliferation and differentiation, and tumorigenesis. Assays for determining whether given homolog of a *p63* exhibits these or other biological activities are known in the art and are further described herein.

In yet another embodiment, the fragment includes the DNA binding domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

In yet another embodiment, the fragment includes the core domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the core domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the core domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

4.3.1 Probes and Primers

The nucleotide sequences determined from the cloning of *p63* genes from mammalian organisms will further allow for the generation of probes and primers designed.

for identifying and/or cloning *p63* homologs in other cell types, e.g., from other tissues, as well as *p63* homologs from other mammalian organisms. For instance, the present invention also provides a probe/primer comprising a substantially purified oligonucleotide, which oligonucleotide comprising a nucleotide sequence that hybridizes under stringent conditions to at least approximately 12, preferably 25, more preferably 40, 50 or 75 consecutive nucleotides of sense or anti-sense sequence selected from the group consisting of SEQ ID No: 1-12 or naturally occurring mutants thereof. For instance, primers based on the nucleic acid represented in SEQ ID NOs:1-12 can be used in PCR reactions to clone *p63* homologs.

In yet another embodiment, the invention provides probes/primers comprising a substantially purified oligonucleotide comprising a nucleotide sequence that hybridizes under moderately stringent conditions to at least approximately 12, 16, 25, 40, 50 or 75 consecutive nucleotides sense or antisense sequence selected from the group consisting of SEQ ID NOS. 1-12, or naturally occurring mutants thereof.

In particular, these probes are useful because they provide a method for detecting mutations in tumor suppressor genes such as *p63, p73, p53* or Rb etc. Nucleic acid probes which are complementary to the wild-type *p63* and can form mismatches with mutant *p63* genes are provided, which allow for detection by enzymatic or chemical cleavage or by shifts in electrophonetic mobility.

Likewise, probes based on the subject *p63* sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins, for use, e.g, in prognostic or diagnostic assays. In preferred embodiments, the probe further comprises a label group attached thereto and able to be detected, e.g., the label group is selected from amongst radioisotopes, fluorescent compounds, enzymes, and enzyme co-factors.

4.3.2 <u>Antisense, Ribozyme and Triplex techniques</u>

Another aspect of the invention relates to the use of the isolated nucleic acid in "antisense" therapy. As used herein, "antisense" therapy refers to administration or *in situ* generation of oligonucleotide molecules or their derivatives which specifically hybridize (e.g., bind) under cellular conditions, with the cellular mRNA and/or genomic DNA encoding one or more of the subject *p63* proteins so as to inhibit expression of that protein, e.g., by inhibiting transcription and/or translation. The binding may be by conventional

base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interactions in the major groove of the double helix. In general, "antisense" therapy refers to the range of techniques generally employed in the art, and includes any therapy which relies on specific binding to oligonucleotide sequences.

An antisense construct of the present invention can be delivered, for example, as an expression plasmid which, when transcribed in the cell, produces RNA which is complementary to at least a unique portion of the cellular mRNA which encodes a *p63* protein. Alternatively, the antisense construct is an oligonucleotide probe which is generated *ex vivo* and which, when introduced into the cell causes inhibition of expression by hybridizing with the mRNA and/or genomic sequences of a *p63* gene. Such oligonucleotide probes are preferably modified oligonucleotides which are resistant to endogenous nucleases, e.g., exonucleases and/or endonucleases, and are therefore stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Patents 5,176,996; 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy have been reviewed, for example, by Van der Krol et al. (1988) BioTechniques 6:958-976; and Stein et al. (1988) Cancer Res 48:2659-2668. With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site, e.g., between the -10 and +10 regions of the *p63* nucleotide sequence of interest, are preferred.

Antisense approaches involve the design of oligonucleotides (either DNA or RNA) that are complementary to *p63* mRNA. The antisense oligonucleotides will bind to the *p63* mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. In the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the mRNA, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the 3' untranslated sequences of mRNAs have recently been shown to be effective at inhibiting

translation of mRNAs as well. (Wagner, R. 1994. Nature 372:333). Therefore, oligonucleotides complementary to either the 5' or 3' untranslated, non-coding regions of a *p63* gene could be used in an antisense approach to inhibit translation of endogenous *p63* mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could also be used in accordance with the invention. Whether designed to hybridize to the 5', 3' or coding region of *p63* mRNA, antisense nucleic acids should be at least six nucleotides in length, and are preferably less that about 100 and more preferably less than about 50, 25, 17 or 10 nucleotides in length.

Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. the oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. W088/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxytiethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine,

5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

The antisense oligonucleotide can also contain a neutral peptide-like backbone. Such molecules are termed peptide nucleic acid (PNA)-oligomers and are described, e.g., in Perry-O'Keefe et al. (1996) Proc. Natl. Acad. Sci. U.S.A. 93:14670 and in Eglom *et al.* (1993) Nature 365:566. One advantage of PNA oligomers is their capability to bind to complementary DNA essentially independently from the ionic strength of the medium due to the neutral backbone of the DNA. In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet a further embodiment, the antisense oligonucleotide is an α-anomeric oligonucleotide. An α-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-0-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-12148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available

from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate olgonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to the *p63* coding region sequence can be used, those complementary to the transcribed untranslated region and to the region comprising the initiating methionine are most preferred.

The antisense molecules can be delivered to cells which express *p63 in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation on endogenous mRNAs. Therefore a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous *p63* transcripts and thereby prevent translation of the *p63* mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto *et al.*, 1980, Cell 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al, 1982, Nature 296:39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced directly into

the tissue site; e.g., the choroid plexus or hypothalamus. Alternatively, viral vectors can be used which selectively infect the desired tissue; (e.g., for brain, herpesvirus vectors may be used), in which case administration may be accomplished by another route (e.g., systematically).

Ribozyme molecules designed to catalytically cleave *p63* mRNA transcripts can also be used to prevent translation of *p63* mRNA and expression of *p63* (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver *et al.*, 1990, Science 247:1222-1225 and U.S. Patent No. 5,093,246). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy *p63* mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, 1988, Nature, 334:585-591. There are a number of potential hammerhead ribozyme cleavage sites within the nucleotide sequence of human *p63* cDNA (Fig. 1). Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the *p63* mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one which occurs naturally in Tetrahymena thermophila (known as the IVS, or L-19 IVS RNA) and which has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224:574-578; Zaug and Cech, 1986, Science, 231:470-475; Zaug, et al., 1986, Nature, 324:429-433; published International patent application No. WO88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47:207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in a *p63* gene.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells which express the *p63* gene *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the robozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to

destroy endogenous *p63* messages and inhibit translation. Because ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous *p63* gene expression can also be reduced by inactivating or "knocking out" the *p63* gene or its promoter using targeted homologous recombination. (E.g., see Smithies *et al.*, 1985, Nature 317:230-234; Thomas & Capecchi, 1987, Cell 51:503-512; Thompson et al., 1989 Cell 5:313-321; each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional *p63* (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous *p63* gene (either the coding regions or regulatory regions of the *p63* gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express *p63 in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the *p63* gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive *p63* (e.g., see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors, e.g., herpes virus vectors for delivery to brain tissue; e.g., the hypothalamus and/or choroid plexus.

Alternatively, endogenous *p63* gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the *p63* gene (i.e., the *p63* promoter and/or enhancers) to form triple helical structures that prevent transcription of the *p63* gene in target cells in the body. (See generally, Helene, C. 1991, Anticancer Drug Des., 6(6):569-84; Helene, C., et al., 1992, Ann, N.Y. Accad. Sci., 660:27-36; and Maher, L.J., 1992, Bioassays 14(12):807-15).

Nucleic acid molecules to be used in triple helix formation for the inhibition of transcription are preferably single stranded and composed of deoxyribonucleotides. The base composition of these oligonucleotides should promote triple helix formation via Hoogsteen base pairing rules, which generally require sizable stretches of either purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-

rich, for example, containing a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in CGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizable stretch of either purines or pyrimidines to be present on one strand of a duplex.

Antisense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

Moreover, various well-known modifications to nucleic acid molecules may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but are not limited to the addition of flanking sequences of ribonucleotides or deoxyribonucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

4.3.3. Vectors Encoding *p63* Proteins and *p63* Expressing Cells

The invention further provides plasmids and vectors encoding an *p63* protein, which can be used to express an *p63* protein in a host cell. The host cell may be any prokaryotic or eukaryotic cell. Thus, a nucleotide sequence derived from the cloning of mammalian *p63* proteins, encoding all or a selected portion of the full-length protein, can be used to produce a recombinant form of an *p63* polypeptide via microbial or eukaryotic cellular processes. Ligating the polynucleotide sequence into a gene construct, such as an expression vector,

and transforming or transfecting into hosts, either eukaryotic (yeast, avian, insect or mammalian) or prokaryotic (bacterial cells), are standard procedures well known in the art.

Vectors that allow expression of a nucleic acid in a cell are referred to as expression vectors. Typically, expression vectors used for expressing an *p63* protein contain a nucleic acid encoding an *p63* polypeptide, operably linked to at least one transcriptional regulatory sequence. Regulatory sequences are art-recognized and are selected to direct expression of the subject *p63* proteins. Transcriptional regulatory sequences are described in Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). In one embodiment, the expression vector includes a recombinant gene encoding a peptide having an agonistic activity of a subject *p63* polypeptide, or alternatively, encoding a peptide which is an antagonistic form of an *p63* protein.

Suitable vectors for the expression of a *p63* polypeptide include plasmids of the types: pBR322-derived plasmids, pEMBL-derived plasmids, pEX-derived plasmids, pBTac-derived plasmids and pUC-derived plasmids for expression in prokaryotic cells, such as *E. coli*.

A number of vectors exist for the expression of recombinant proteins in yeast. For instance, YEP24, YIP5, YEP51, YEP52, pYES2, and YRP17 are cloning and expression vehicles useful in the introduction of genetic constructs into S. cerevisiae (see, for example, Broach *et al.* (1983) in Experimental Manipulation of Gene Expression, ed. M. Inouye Academic Press, p. 83, incorporated by reference herein). These vectors can replicate in E. coli due the presence of the pBR322 ori, and in S. cerevisiae due to the replication determinant of the yeast 2 micron plasmid. In addition, drug resistance markers such as ampicillin can be used. In an illustrative embodiment, a *p63* polypeptide is produced recombinantly utilizing an expression vector generated by sub-cloning the coding sequence of one of the *p63* genes represented in SEQ ID NOs:1 or 3.

The preferred mammalian expression vectors contain both prokaryotic sequences, to facilitate the propagation of the vector in bacteria, and one or more eukaryotic transcription units that are expressed in eukaryotic cells. The pcDNAI/amp, pcDNAI/neo, pRc/CMV, pSV2gpt, pSV2neo, pSV2-dhfr, pTk2, pRSVneo, pMSG, pSVT7, pko-neo and pHyg derived vectors are examples of mammalian expression vectors suitable for transfection of eukaryotic cells. Some of these vectors are modified with sequences from bacterial plasmids, such as pBR322, to facilitate replication and drug resistance selection in both prokaryotic and eukaryotic cells. Alternatively, derivatives of viruses such as the bovine papillomavirus (BPV-1), or Epstein-Barr virus (pHEBo, pREP-derived and p205)

can be used for transient expression of proteins in eukaryotic cells. The various methods employed in the preparation of the plasmids and transformation of host organisms are well known in the art. For other suitable expression systems for both prokaryotic and eukaryotic cells, as well as general recombinant procedures, see Molecular Cloning A Laboratory Manual, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989) Chapters 16 and 17.

In some instances, it may be desirable to express the recombinant *p63* polypeptide by the use of a baculovirus expression system. Examples of such baculovirus expression systems include pVL-derived vectors (such as pVL1392, pVL1393 and pVL941), pAcUW-derived vectors (such as pAcUW1), and pBlueBac-derived vectors (such as the ß-gal containing pBlueBac III)

When it is desirable to express only a portion of a *p63* protein, such as a form lacking a portion of the N-terminus, i.e. a truncation mutant which lacks the signal peptide, it may be necessary to add a start codon (ATG) to the oligonucleotide fragment containing the desired sequence to be expressed. It is well known in the art that a methionine at the N-terminal position can be enzymatically cleaved by the use of the enzyme methionine aminopeptidase (MAP). MAP has been cloned from E. coli (Ben-Bassat *et al.* (1987) J. Bacteriol. 169:751-757) and Salmonella typhimurium and its *in vitro* activity has been demonstrated on recombinant proteins (Miller *et al.* (1987) PNAS 84:2718-1722). Therefore, removal of an N-terminal methionine, if desired, can be achieved either *in vivo* by expressing *p63* derived polypeptides in a host which produces MAP (e.g., E. coli or CM89 or S. cerevisiae), or *in vitro* by use of purified MAP (e.g., procedure of Miller *et al.*, *supra*).

Moreover, the gene constructs of the present invention can also be used as part of a gene therapy protocol to deliver nucleic acids encoding either an agonistic or antagonistic form of one of the subject *p63* proteins. Thus, another aspect of the invention features expression vectors for *in vivo* or *in vitro* transfection and expression of a *p63* polypeptide in particular cell types so as to reconstitute the function of, or alternatively, abrogate the function of *p63* in a tissue. This could be desirable, for example, when the naturally-occurring form of the protein is misexpressed or the natural protein is mutated and less active.

In addition to viral transfer methods, non-viral methods can also be employed to cause expression of a subject *p63* polypeptide in the tissue of an animal. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the

uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral targeting means of the present invention rely on endocytic pathways for the uptake of the subject *p63* polypeptide gene by the targeted cell. Exemplary targeting means of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

In other embodiments transgenic animals, described in more detail below could be used to produce recombinant proteins.

4.4. Polypeptides of the Present Invention

The present invention makes available isolated *p63* polypeptides which are isolated from, or otherwise substantially free of other cellular proteins, especially other signal transduction factors and/or transcription factors which may normally be associated with the *p63* polypeptide. The term "substantially free of other cellular proteins" (also referred to herein as "contaminating proteins") or "substantially pure or purified preparations" are defined as encompassing preparations of *p63* polypeptides having less than about 20% (by dry weight) contaminating protein, and preferably having less than about 5% contaminating protein. Functional forms of the subject polypeptides can be prepared, for the first time, as purified preparations by using a cloned gene as described herein. Full length proteins or fragments corresponding to one or more particular motifs and/or domains or to arbitrary sizes, for example, at least 5, 10, 25, 50, 75 and 100, amino acids in length are within the scope of the present invention.

In yet another embodiment, the fragment includes the core domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the core domain of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the core domain of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

In yet another embodiment, the fragment includes the DNA binding domain of *p63* and comprises at least 5 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding of *p63* and comprises at least 20 contiguous amino acid residues of SEQ ID Nos. 13-24; the fragment includes the DNA binding of *p63* and comprises at least 50 contiguous amino acid residues of SEQ ID Nos. 13-24.

For example, isolated *p63* polypeptides can be encoded by all or a portion of a nucleic acid sequence shown in any of SEQ ID NOS. 1-12. Isolated peptidyl portions of *p63* proteins can be obtained by screening peptides recombinantly produced from the corresponding fragment of the nucleic acid encoding such peptides. In addition, fragments

can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, a *p63* polypeptide of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or preferably divided into overlapping fragments of a desired length. The fragments can be produced (recombinantly or by chemical synthesis) and tested to identify those peptidyl fragments which can function as either agonists or antagonists of a wild-type (e.g., "authentic") *p63* protein.

Another aspect of the present invention concerns recombinant forms of the *p63* proteins. Recombinant polypeptides preferred by the present invention, in addition to native *p63* proteins (e.g., as set forth in SEQ ID NO: 6), are encoded by a nucleic acid, which is at least 60 %, more preferably at least 80%, and more preferably 85%, and more preferably 90%, and more preferably 95 % identical to an amino acid sequence represented by SEQ ID Nos: 13-24 or encoded by SEQ ID NOs. 13-24. Polypeptides which are encoded by a nucleic acid that is at least about 98-99% identical with the sequence of SEQ ID NOS: 1 or 3 or which are 98-99% identical with the amino acid sequence set forth in SEQ ID NO: 2 are also within the scope of the invention.

In a preferred embodiment, a *p63* protein of the present invention is a mammalian *p63* protein and even more preferably a human *p63* protein. In a particularly preferred embodiment the *p63* protein has an amino acid sequence as set forth in SEQ ID Nos: 13-24. In particularly preferred embodiment, the *p63* protein retains *p63* bioactivity. It will be understood that certain post-translational modifications, e.g., phosphorylation and the like, can increase the apparent molecular weight of the *p63* protein relative to the unmodified polypeptide chain.

The present invention further pertains to recombinant forms of one of the subject *p63* polypeptides. Such recombinant *p63* polypeptides preferably are capable of functioning in one of either role of an agonist or antagonist of at least one biological activity of a wild-type ("authentic") *p63* protein of the appended sequence listing. The term "evolutionarily related to", with respect to amino acid sequences of *p63* proteins, refers to both polypeptides having amino acid sequences which have arisen naturally, and also to mutational variants of human *p63* polypeptides which are derived, for example, by combinatorial mutagenesis.

In general, polypeptides referred to herein as having an activity (e.g., are "bioactive") of a *p63* protein are defined as polypeptides which include an amino acid sequence encoded by all or a portion of the nucleic acid sequences shown in one of SEQ ID NOS: 1-12 and which mimic or antagonize all or a portion of the biological/biochemical activities of a

naturally occurring *p63* protein. Preferred bioactive fragments of *p63* polypeptides include polypeptides having one or more of the following biological activities: activity as a tumor suppressor, functions in cell cycle control various developmental processes, apoptosis, gene expression and tumorigenesis. Other biological activities of the subject *p63* proteins are described herein or will be reasonably apparent to those skilled in the art. According to the present invention, a polypeptide has biological activity if it is a specific agonist or antagonist of a naturally-occurring form of a *p63* protein.

Assays for determining whether a compound, e.g, a protein, such as an *p63* protein or variant thereof, has one or more of the above biological activities are well known in the art.

In another embodiment, the coding sequences for the polypeptide can be incorporated as a part of a fusion gene including a nucleotide sequence encoding a different polypeptide. This type of expression system can be useful under conditions where it is desirable to produce an immunogenic fragment of a *p63* protein. For example, the VP6 capsid protein of rotavirus can be used as an immunologic carrier protein for portions of the *p63* polypeptide, either in the monomeric form or in the form of a viral particle. The nucleic acid sequences corresponding to the portion of a subject *p63* protein to which antibodies are to be raised can be incorporated into a fusion gene construct which includes coding sequences for a late vaccinia virus structural protein to produce a set of recombinant viruses expressing fusion proteins comprising *p63* epitopes as part of the virion. It has been demonstrated with the use of immunogenic fusion proteins utilizing the Hepatitis B surface antigen fusion proteins that recombinant Hepatitis B virions can be utilized in this role as well. Similarly, chimeric constructs coding for fusion proteins containing a portion of a *p63*protein and the poliovirus capsid protein can be created to enhance immunogenicity of the set of polypeptide antigens (see, for example, EP Publication No: 0259149; and Evans *et al.* (1989) Nature 339:385; Huang *et al.* (1988) J. Virol. 62:3855; and Schlienger *et al.* (1992) J. Virol. 66:2).

The Multiple antigen peptide system for peptide-based immunization can also be utilized to generate an immunogen, wherein a desired portion of a *p63* polypeptide is obtained directly from organo-chemical synthesis of the peptide onto an oligomeric branching lysine core (see, for example, Posnett et al. (1988) JBC 263:1719 and Nardelli *et al.* (1992) J. Immunol. 148:914). Antigenic determinants of *p63* proteins can also be expressed and presented by bacterial cells.

In addition to utilizing fusion proteins to enhance immunogenicity, it is widely appreciated that fusion proteins can also facilitate the expression of proteins, and accordingly, can be used in the expression of the *p63* polypeptides of the present invention. For example, *p63* polypeptides can be generated as glutathione-S-transferase (GST-fusion) proteins. Such GST-fusion proteins can enable easy purification of the *p63* polypeptide, as for example by the use of glutathione-derivatized matrices (see, for example, Current Protocols in Molecular Biology, eds. Ausubel et al. (N.Y.: John Wiley & Sons, 1991)).

In another embodiment, a fusion gene coding for a purification leader sequence, such as a poly-(His)/enterokinase cleavage site sequence at the N-terminus of the desired portion of the recombinant protein, can allow purification of the expressed fusion protein by affinity chromatography using a Ni^{2+} metal resin. The purification leader sequence can then be subsequently removed by treatment with enterokinase to provide the purified protein (e.g., see Hochuli *et al.* (1987) J. Chromatography 411:177; and Janknecht *et al.* PNAS 88:8972). Techniques for making fusion genes are known to those skilled in the art. Essentially, the joining of various DNA fragments coding for different polypeptide sequences is performed in accordance with conventional techniques, employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed to generate a chimeric gene sequence (see, for example, Current Protocols in Molecular Biology, eds. Ausubel et al. John Wiley & Sons: 1992).

The present invention further pertains to methods of producing the subject *p63* polypeptides. For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding the subject polypeptides can be cultured under appropriate conditions to allow expression of the peptide to occur. Suitable media for cell culture are well known in the art. The recombinant *p63* polypeptide can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such peptide. In a preferred embodiment, the recombinant *p63* polypeptide is a fusion protein containing a domain which facilitates its purification, such as GST fusion protein.

Moreover, it will be generally appreciated that, under certain circumstances, it may be advantageous to provide homologs of one of the subject *p63* polypeptides which function in a limited capacity as one of either a *p63* agonist (mimetic) or a *p63* antagonist, in order to promote or inhibit only a subset of the biological activities of the naturally-occurring form of the protein. Thus, specific biological effects can be elicited by treatment with a homolog of limited function, and with fewer side effects relative to treatment with agonists or antagonists which are directed to all of the biological activities of naturally occurring forms of *p63* proteins.

Homologs of each of the subject *p63* proteins can be generated by mutagenesis, such as by discrete point mutation(s), or by truncation. For instance, mutation can give rise to homologs which retain substantially the same, or merely a subset, of the biological activity of the *p63* polypeptide from which it was derived. Alternatively, antagonistic forms of the protein can be generated which are able to inhibit the function of the naturally occurring form of the protein, such as by competitively binding to an *p63* receptor.

The recombinant *p63* polypeptides of the present invention also include homologs of the wildtype *p63* proteins, such as versions of those protein which are resistant to proteolytic cleavage, as for example, due to mutations which alter ubiquitination or other enzymatic targeting associated with the protein.

p63 polypeptides may also be chemically modified to create *p63* derivatives by forming covalent or aggregate conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of *p63* proteins can be prepared by linking the chemical moieties to functional groups on amino acid sidechains of the protein or at the N-terminus or at the C-terminus of the polypeptide.

Modification of the structure of the subject *p63* polypeptides can be for such purposes as enhancing therapeutic or prophylactic efficacy, stability (e.g., *ex vivo* shelf life and resistance to proteolytic degradation), or post-translational modifications (e.g., to alter phosphorylation pattern of protein). Such modified peptides, when designed to retain at least one activity of the naturally-occurring form of the protein, or to produce specific antagonists thereof, are considered functional equivalents of the *p63* polypeptides described in more detail herein. Such modified peptides can be produced, for instance, by amino acid substitution, deletion, or addition. The substitutional variant may be a substituted conserved amino acid or a substituted non-conserved amino acid.

For example, it is reasonable to expect that an isolated replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar

replacement of an amino acid with a structurally related amino acid (i.e. isosteric and/or isoelectric mutations) will not have a major effect on the biological activity of the resulting molecule. Conservative replacements are those that take place within a family of amino acids that are related in their side chains. Genetically encoded amino acids can be divided into four families: (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine, histidine; (3) nonpolar = alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar = glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine. In similar fashion, the amino acid repertoire can be grouped as (1) acidic = aspartate, glutamate; (2) basic = lysine, arginine histidine, (3) aliphatic = glycine, alanine, valine, leucine, isoleucine, serine, threonine, with serine and threonine optionally be grouped separately as aliphatic-hydroxyl; (4) aromatic = phenylalanine, tyrosine, tryptophan; (5) amide = asparagine, glutamine; and (6) sulfur -containing = cysteine and methionine. (see, for example, Biochemistry, 2nd ed., Ed. by L. Stryer, WH Freeman and Co.: 1981). Whether a change in the amino acid sequence of a peptide results in a functional *p63* homolog (e.g., functional in the sense that the resulting polypeptide mimics or antagonizes the wild-type form) can be readily determined by assessing the ability of the variant peptide to produce a response in cells in a fashion similar to the wild-type protein, or competitively inhibit such a response. Polypeptides in which more than one replacement has taken place can readily be tested in the same manner.

This invention further contemplates a method for generating sets of combinatorial mutants of the subject *p63* proteins as well as truncation mutants, and is especially useful for identifying potential variant sequences (e.g., homologs). The purpose of screening such combinatorial libraries is to generate, for example, novel *p63* homologs which can act as either agonists or antagonist, or alternatively, possess novel activities all together. Thus, combinatorially-derived homologs can be generated to have an increased potency relative to a naturally occurring form of the protein.

In one embodiment, the variegated library of *p63* variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For instance, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential *p63* sequences are expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of *p63* sequences therein. There are many ways by which such libraries of potential *p63* homologs can be generated from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be carried out in an

automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The purpose of a degenerate set of genes is to provide, in one mixture, all of the sequences encoding the desired set of potential *p63 s*equences. The synthesis of degenerate oligonucleotides is well known in the art (see for example, Narang, SA (1983) Tetrahedron 39:3; Itakura *et al.* (1981) Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules, ed. AG Walton, Amsterdam: Elsevier pp 273-289; Itakura et al. (1984) Annu. Rev. Biochem. 53:323; Itakura *et al.* (1984) Science 198:1056; Ike et al. (1983) Nucleic Acid Res. 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) Science 249:386-390; Roberts et al. (1992) PNAS 89:2429-2433; Devlin *et al.* (1990) Science 249: 404-406; Cwirla et al. (1990) PNAS 87: 6378-6382; as well as U.S. Patents NOS. 5,223,409, 5,198,346, and 5,096,815).

Likewise, a library of coding sequence fragments can be provided for a *p63*clone in order to generate a variegated population of *p63* fragments for screening and subsequent selection of bioactive fragments. A variety of techniques are known in the art for generating such libraries, including chemical synthesis. In one embodiment, a library of coding sequence fragments can be generated by (i) treating a double stranded PCR fragment of a *p63*coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule; (ii) denaturing the double stranded DNA; (iii) renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products; (iv) removing single stranded portions from reformed duplexes by treatment with S1 nuclease; and (v) ligating the resulting fragment library into an expression vector. By this exemplary method, an expression library can be derived which codes for N-terminal, C-terminal and internal fragments of various sizes.

A wide range of techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a certain property. Such techniques will be generally adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of *p63* homologs. The most widely used techniques for screening large gene libraries typically comprises cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the illustrative assays described below are amenable to high through-put analysis as

necessary to screen large numbers of degenerate *p63* sequences created by combinatorial mutagenesis techniques. Combinatorial mutagenesis has a potential to generate very large libraries of mutant proteins, e.g., in the order of 10^{26} molecules. Combinatorial libraries of this size may be technically challenging to screen even with high throughput screening assays. To overcome this problem, a new technique has been developed recently, recrusive ensemble mutagenesis (REM), which allows one to avoid the very high proportion of non-functional proteins in a random library and simply enhances the frequency of functional proteins, thus decreasing the complexity required to achieve a useful sampling of sequence space. REM is an algorithm which enhances the frequency of functional mutants in a library when an appropriate selection or screening method is employed (Arkin and Yourvan, 1992, PNAS USA 89:7811-7815; Yourvan *et al.*, 1992, Parallel Problem Solving from Nature, 2., In Maenner and Manderick, eds., Elsevir Publishing Co., Amsterdam, pp. 401-410; Delgrave et al., 1993, Protein Engineering 6(3):327-331).

The invention also provides for reduction of the *p63* proteins to generate mimetics, e.g., peptide or non-pepide agents, such as small molecules, which are able to disrupt binding of a *p63* polypeptide of the present invention with a nucleotide, such as proteins, e.g. receptors. Thus, such mutagenic techniques as described above are also useful to map the determinants of the *p63* proteins which participate in protein-protein interactions involved in, for example, binding of the subject *p63* polypeptide to a target peptide. To illustrate, the critical residues of a subject *p63* polypeptide which are involved in molecular recognition of its receptor can be determined and used to generate *p63* derived peptidomimetics or small molecules which competitively inhibit binding of the authentic *p63* protein with that moiety. By employing, for example, scanning mutagenesis to map the amino acid residues of the subject *p63* proteins which are involved in binding other proteins, peptidomimetic compounds can be generated which mimic those residues of the *p63* protein which facilitate the interaction. Such mimetics may then be used to interfere with the normal function of a *p63* protein. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger *et al.* in Peptides: Chemistry and Biology, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in Peptides: Chemistry and Biology, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in Peptides: Chemistry and Biology, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson *et al.* (1986) J Med Chem 29:295; and Ewenson et al. in Peptides: Structure and Function (Proceedings of the 9th

American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), β-turn dipeptide cores (Nagai et al. (1985) Tetrahedron Lett 26:647; and Sato et al. (1986) J Chem Soc Perkin Trans 1:1231), and β-aminoalcohols (Gordon et al. (1985) Biochem Biophys Res Commun126:419; and Dann et al. (1986) Biochem Biophys Res Commun 134:71).

4.5. Anti-*p63* Antibodies and Uses Therefor

Another aspect of the invention pertains to an antibody specifically reactive with a mammalian *p63* protein, e.g., a wild-type or mutated *p63* protein. For example antibodies may be made as described in teh appended rxamples or by using other standard protocols (See, for example, Antibodies: A Laboratory Manual ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal, such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide (e.g., a mammalian *p63* polypeptide or an antigenic fragment which is capable of eliciting an antibody response, or a fusion protein as described above).

In one aspect, this invention includes monoclonal antibodies to *p63* that show *p63* is highly expressed in the basal cells of various epithelial tissues, including epidermis, ectocervical epithelium, vaginal epithelium, urothelium, and prostate epthelium, all of which represent common sites of human carcinomas (basal cell carcinoma of skin, cervical carcinoma with and without human papilloma virus association, bladder and urothelial carcinoma, and prostate carcinoma). Therefore, in one embodiment this invention provides a diagnostic tool for the analysis of *p63* expression in general, and in particular, as a diagnostic for analysis of carcinomas.

Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of a *p63* protein can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies. In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of a *p63* protein of a mammal, e.g., antigenic determinants of a protein set forth in SEQ ID No: 2 or closely related homologs (e.g., at least 90% identical, and more preferably at least 95% identical).

Following immunization of an animal with an antigenic preparation of a *p63* polypeptide, anti- *p63* antisera can be obtained and, if desired, polyclonal anti- *p63* antibodies isolated from the serum. To produce monoclonal antibodies, antibody-producing

cells (lymphocytes) can be harvested from an immunized animal and fused by standard somatic cell fusion procedures with immortalizing cells such as myeloma cells to yield hybridoma cells. Such techniques are well known in the art, and include, for example, the hybridoma technique (originally developed by Kohler and Milstein, (1975) Nature, 256: 495-497), the human B cell hybridoma technique (Kozbar *et al.*, (1983) Immunology Today, 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., (1985) Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. pp. 77-96). Hybridoma cells can be screened immunochemically for production of antibodies specifically reactive with a mammalian *p63* polypeptide of the present invention and monoclonal antibodies isolated from a culture comprising such hybridoma cells. In one embodiment anti-human *p63* antibodies specifically react with the protein encoded by the DNA of ATCC deposit No.________.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with one of the subject mammalian *p63* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, $F(ab)_2$ fragments can be generated by treating antibody with pepsin. The resulting $F(ab)_2$ fragment can be treated to reduce disulfide bridges to produce Fab fragments. The antibody of the present invention is further intended to include bispecific, single-chain, and chimeric and humanized molecules having affinity for a *p63* protein conferred by at least one CDR region of the antibody. In preferred embodiments, the antibodies, the antibody further comprises a label attached thereto and able to be detected, (e.g., the label can be a radioisotope, fluorescent compound, enzyme or enzyme co-factor).

Anti-*p63* antibodies can be used, e.g., to monitor *p63* protein levels in an individual for determining, e.g., whether a subject has a disease or condition associated with an aberrant *p63* protein level, or allowing determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of *p63* polypeptides may be measured from cells in bodily fluid, such as in blood samples.

Another application of anti-*p63* antibodies of the present invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λgt11, λgt18-23, λZAP, and λORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λgt11 will produce fusion proteins whose amino termini consist of ß-galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide.

Antigenic epitopes of a *p63* protein, e.g., other orthologs of a particular *p63* protein or other paralogs from the same species, can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*p63* antibodies. Positive phage detected by this assay can then be isolated from the infected plate. Thus, the presence of *p63* homologs can be detected and cloned from other animals, as can alternate isoforms (including splicing variants) from humans.

In another embodiment, a panel of monoclonal antibodies may be used, wherein each of the epitopes involved *p63* functions are represented by a monoclonal antibody. Loss or perturbation of binding of a monoclonal antibody in the panel would be indicative of a mutational attention of the *p63* protein and thus of the *p63* gene.

4.6. Transgenic animals

One aspect of the present invention relates to transgenic non-human animals having germline and/or somatic cells in which the biological activity of one or more tumor supressor genes, e.g., *p63*, p53, p73 proteins, combinations thereof, are altered by a chromosomally incorporated transgene.

In one preferred embodiment, the transgene disrupts at least a portion of a genomic *p63* gene. For instance, the transgene may delete all or a portion of the genomic *p63* gene by replacement recombination, or may functionally interrupt one or more of a regulatory sequence or coding sequence of the genomic *p63* gene by insertion recombination.

In another preferred embodiment, the transgene encodes a *p63* protein, and expression of the transgene in cells of the transgenic animal results in altered regulation of the level of the *p63* protein relative to normal expression of the wild-type *p63* protein.

In still other preferred embodiments, the transgene encodes a mutant *p63* protein, such as dominant negative *p63* protein which antagonizes at least a portion of the biological function of a wild-type *p63* protein.

Yet another preferred transgenic animal includes a transgene encoding an antisense transcript which, when transcribed from the transgene, hybridizes with a genomic *p63* gene or a mRNA transcript thereof, and inhibits expression of the genomic *p63* gene.

In one embodiment, the present invention provides a desired non-human animal or an animal (including human) cell which contains a predefined, specific and desired alteration rendering the non-human animal or animal cell predisposed to cancer. Specifically, the

invention pertains to a genetically altered non-human animal (most preferably, a mouse), or a cell (either non-human animal or human) in culture, that is defective in at least one of two alleles of a tumor-suppressor gene such as the *p63* gene. The inactivation of at least one of these tumor suppressor alleles results in an animal with a higher susceptibility to tumor inductionor other proliferative or differentiative disorders, or disorders marked by abberrant signal transduction, e/g/, from a cytokine or growth factor. A genetically altered mouse of this type is able to serve as a useful model for hereditary cancers and as a test animal for carcinogen studies. The invention additionally pertains to the use of such non-human animals or animal cells, and their progeny in research and medicine.

Furthermore, it is contemplated that cells of the transgenic animals of the present invention can include other transgenes, e.g., which alter the biological activity of a second tumor suppressor gene or an oncogene. For instance, the second transgene can functionally disrupt the biological activity of a second tumor suppressor gene, such as p53, p73, DCC, $p21^{cip1}$, $p27^{kip1}$, Rb, Mad or E2F. Alternatively, the second transgene can cause overexpression or loss of regulation of an oncogene, such as ras, myc, a cdc25 phosphatase, Bcl-2, Bcl-6, a transforming growth factor, neu, int-3, polyoma virus middle T antigen, SV40 large T antigen, a papillomaviral E6 protein, a papillomaviral E7 protein, CDK4, or cyclin D1.

A preferred transgenic non-human animal of the present invention has germline and/or somatic cells in which one or more alleles of a genomic *p63* gene, a p73 gene, a p53 gene, and combinations thereof, are disrupted by a chromosomally incorporated transgene, wherein the transgene includes a marker sequence providing a detectable signal for identifying the presence of the transgene in cells of the transgenic animal, and replaces at least a portion of the genomic *p63* gene or is inserted into the genomic *p63* gene or disrupt expression of a wild type *p63* protein.

Another aspect of the present invention relates to cells and tissues isolated from the subject transgenic animals. For instance, the present invention provides composition of cells, isolated *ex vivo*, which include a diploid genome having a chromosomally incorporated transgene, which transgene functionally modifies the biological activity of one or more *p63* proteins. In preferred embodiments, the transgene deletes all or a portion of a genomic *p63* gene by replacement recombination, or functionally interrupts one or more of a regulatory sequence or coding sequence of the genomic *p63* gene by insertion recombination. For instance, one class of such cells contemplated by the present invention include transgenes

which have (i) at least a portion of the genomic *p63* gene which directs recombination of the transgene with the genomic *p63* gene, and (ii) a marker sequence which provides a detectable signal for identifying the presence of the transgene in a cell.

The animals of this invention can be used as a source of cells, differentiated or precursor, which can be immortalized in cell culture. In a preferred embodiment, the cells are stem cells or pluripotent progenitor cells. For instance, such cells can be precursors of hematopoietic cells, neuronal cells, pancreatic cells, hepatic cells, chondrocytes, osteocytes, myocytes, or combinations thereof.

Still another aspect of the present invention relates to methods for generating non-human animals and stem cells having a functionally disrupted endogenous *p63* gene. In a preferred embodiment, the method comprises the steps of:

(i) constructing a transgene construct including (a) a recombination region having at least a portion of the *p63* gene, which recombination region directs recombination of the transgene with the *p63* gene, and (b) a marker sequence which provides a detectable signal for identifying the presence of the transgene in a cell;

(ii) transfering the transgene into stem cells of a non-human animal;

(iii) selecting stem cells having a correctly targeted homologous recombination between the transgene and the *p63* gene;

(iv) transfering cells identified in step (iii) into a non-human blastocyst and implanting the resulting chimeric blastocyst into a non-human female; and

(v) collecting offspring harboring an endogenous *p63* gene allele having the correctly targeted recombinantion.

Yet another aspect of the invention provides a method for evaluating the carcinogenic potential of an agent by (i) contacting a transgenic animal of the present invention with a test agent, and (ii) comparing the number of transformed cells in a sample from the treated animal with the number of transformed cells in a sample from an untreated transgenic animal or transgenic animal treated with a control agent. The difference in the number of transformed cells in the treated animal, relative to the number of transformed cells in the absence of treatment with a control agent, indicates the carcinogenic potential of the test compound.

Another aspect of the invention provides a method of evaluating an anti-proliferative activity of a test compound. In preferred embodiments, the method includes contacting a

transgenic animal of the present invention, or a sample of cells from such animal, with a test agent, and determining the number of transformed cells in a specimen from the transgenic animal or in the sample of cells. A statistically significant decrease in the number of transformed cells, relative to the number of transformed cells in the absence of the test agent, indicates the test compound is a potential anti-proliferative agent.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press:1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis *et al.* U.S. Patent No. 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu et al. eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); *Handbook Of Experimental Immunology*, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); *Manipulating the Mouse Embryo*, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

4.7 Screening Assays for *p63* Therapeutics

The invention provides for *p63* therapeutic compounds for treating diseases or conditions caused by, or contributed to by an abnormal *p63* activity, e.g., a predisposition to form tumors. The compounds that can be used for this purpose can be any type of compound, including a protein, a peptide, peptidomimetic, small molecule, and nucleic acid. A nucleic acid can be, e.g., a gene, an antisense nucleic acid, a ribozyme, or a triplex molecule. A compound of the invention can be an agonist or an antagonist. Preferred *p63* agonists include *p63* proteins or derivatives thereof which mimic at least one *p63* activity, e.g., the ability to activate transcription, act as a tumor suppressor, inhibit tumorigenesis by eliminating potentially tumorigeale cells hydrolysis of a target peptide or nucleic acids

encoding such. Other preferred agonists include compounds which are capable of increasing the production of *p63* protein in cells, e.g., compounds capable of upregulating the expression of a *p63* gene. Preferred *p63* antagonists include compounds which decrease or inhibit interaction of a *p63* protein with a target gene. In a preferred embodiment, a *p63* antagonist is a modified form of a target peptide, which is capable of interacting with the target gene, but which does not have biological activity, e.g., will not act as a transcription factor.

It is possible that when *p63* functions as a transcription factor, it uses its central domain to bind to its target sequence. This region of *p63* may also b a target for other proteins that interact with it. These proteins, could increase or decrease transactivation. Accordingly, compounds modulating the interaction of such proteins with *p63* could be agonists or antagonists.

Thus, the invention provides methods for identifying *p63* agonist and antagonist compounds, comprising selecting compounds which are capable of modulating the interaction of an *p63* protein with another molecule referred to herein as "*p63* binding partner". A *p63* binding partner can be a target gene or a target oncoprotein etc. A *p63* binding partner can also be a polypeptide which is not a target peptide and which may, e.g., interact with a *p63* protein at sites other than its major binding domain. In yet other embodiments of the invention, an *p63* therapeutic is a compound which is capable of binding to a *p63* protein, e.g., a wild-type *p63* protein or a mutated form of a *p63* protein, and thereby modulate the catalytic activity of the *p63*-protein or degrade or cause the *p63* protein to be degraded. For example, such an *p63* therapeutic can be an antibody or derivative thereof which interacts specifically with an *p63* protein (either wild-type or mutated).

In a further embodiment, the *p63* therapeutic of the invention is capable of acting on an *p63* gene, e.g., to modulate its expression.

The compounds of the invention can be identified using various assays depending on the type of compound and activity of the compound that is desired. Set forth below are at least some assays that can be used for identifying *p63* therapeutics. It is within the skill of the art to design additional assays for identifying *p63* therapeutics.

4.7.1 <u>Cell-free assays</u>

Cell-free assays can be used to identify compounds which modulate the interaction between an *p63* protein and a *p63* binding partner, such as a target gene or peptide. In a preferred embodiment, cell-free assays for identifying such compounds consist essentially

in combining together in a reaction mixture a *p63* protein, a *p63* binding partner and a test compound or a library of test compounds. A test compound can be a derivative of a *p63* binding partner, e.g., an biologically inactive target peptide, or the test compound can be a small molecule.

Accordingly, an exemplary screening assay of the present invention includes the steps of (a) forming a reaction mixture including: (i) a *p63* polypeptide, (ii) a *p63* binding partner (e.g., *p21* such as a target gene, examples include activation of *p21*, which exhibits the cell cycle and/or GADD45 a repair protein activated by pathways that respond to irradiation damage), and (iii) a test compound; and (b) detecting interaction of the *p63* and the *p63* binding protein. The *p63* polypeptide and *p63* binding partner can be produced recombinantly, purified from a source, e.g., plasma, or chemically synthesized, as described herein. A statistically significant change (potentiation or inhibition) in the interaction of the *p63* and *p63* binding protein in the presence of the test compound, relative to the interaction in the absence of the test compound, indicates a potential agonist (mimetic or potentiator) or antagonist (inhibitor) of *p63* bioactivity for the test compound. The compounds of this assay can be contacted simultaneously. Alternatively, a *p63* protein can first be contacted with a test compound for an appropriate amount of time, following which the *p63* binding partner is added to the reaction mixture. The efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. In the control assay, isolated and purified *p63* polypeptide or binding partner is added to a composition containing the *p63* binding partner or *p63* polypeptide, and the formation of a complex is quantitated in the absence of the test compound.

Complex formation between a *p63* protein and a *p63* binding partner may be detected by a variety of techniques. Modulation of the formation of complexes can be quantitated using, for example, detectably labeled proteins such as radiolabeled, fluorescently labeled, or enzymatically labeled *p63* proteins or *p63* binding partners, by immunoassay, or by chromatographic detection.

Typically, it will be desirable to immobilize either *p63* or its binding partner to facilitate separation of complexes from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of *p63* to a *p63* binding partner, can be accomplished in any vessel suitable for containing the reactants. Examples include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows the protein to be bound to

a matrix. For example, glutathione-S-transferase/*p63* (GST/*p63*) fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtitre plates, which are then combined with the *p63* binding partner, e.g. an ^{35}S-labeled *p63* binding partner, and the test compound, and the mixture incubated under conditions conducive to complex formation, e.g. at physiological conditions for salt and pH, though slightly more stringent conditions may be desired. Following incubation, the beads are washed to remove any unbound label, and the matrix immobilized and radiolabel determined directly (e.g. beads placed in scintilant), or in the supernatant after the complexes are subsequently dissociated. Alternatively, the complexes can be dissociated from the matrix, separated by SDS-PAGE, and the level of *p63* protein or *p63* binding partner found in the bead fraction quantitated from the gel using standard electrophoretic techniques such as described in the appended examples.

Other techniques for immobilizing proteins on matrices are also available for use in the subject assay. For instance, either *p63* or its cognate binding partner can be immobilized utilizing conjugation of biotin and streptavidin. For instance, biotinylated *p63* molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with *p63* can be derivatized to the wells of the plate, and *p63* trapped in the wells by antibody conjugation. As above, preparations of a *p63* binding protein and a test compound are incubated in the *p63* presenting wells of the plate, and the amount of complex trapped in the well can be quantitated. Exemplary methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the *p63* binding partner, or which are reactive with *p63* protein and compete with the binding partner; as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the binding partner, either intrinsic or extrinsic activity. In the instance of the latter, the enzyme can be chemically conjugated or provided as a fusion protein with the *p63* binding partner. To illustrate, the *p63* binding partner can be chemically cross-linked or genetically fused with horseradish peroxidase, and the amount of polypeptide trapped in the complex can be assessed with a chromogenic substrate of the enzyme, e.g. 3,3'-diamino-benzadine terahydrochloride or 4-chloro-1-napthol. Likewise, a fusion protein comprising the polypeptide and glutathione-S-transferase can be provided, and complex formation

quantitated by detecting the GST activity using 1-chloro-2,4-dinitrobenzene (Habig et al (1974) J Biol Chem 249:7130).

For processes which rely on immunodetection for quantitating one of the proteins trapped in the complex, antibodies against the protein, such as anti-*p63* antibodies, can be used. Alternatively, the protein to be detected in the complex can be "epitope tagged" in the form of a fusion protein which includes, in addition to the *p63* sequence, a second polypeptide for which antibodies are readily available (e.g. from commercial sources). For instance, the GST fusion proteins described above can also be used for quantification of binding using antibodies against the GST moiety. Other useful epitope tags include myc-epitopes (e.g., see Ellison et al. (1991) J Biol Chem 266:21150-21157) which includes a 10-residue sequence from c-myc, as well as the pFLAG system (International Biotechnologies, Inc.) or the pEZZ-protein A system (Pharamacia, NJ).

Cell-free assays can also be used to identify compounds which interact with a *p63* protein and modulate an activity of a *p63* protein. Accordingly, in one embodiment, a *p63* protein is contacted with a test compound and the actual transcription of a target gene activity of *p63* is monitored. In one embodiment, the abililty of *p63* to bind to and/or to hydrolyze a target peptide, e.g, angiotensin I or a kinin, such as bradykinin is determined. The binding affinity of *p63* to a target peptide can be determined according to methods known in the art. Determination of the enzymatic activity of *p63* can be performed with the aid of the substrate furanacryloyl-L-phenylalanyl-glycyl-glycine (FAPGG) under conditions described in Holmquist et al. (1979) Anal. Biochem. 95:540 and in U.S. Patent No. 5,259,045. The subject screening assays can be accomplished in any vessel suitable for containing the reactants. Examples include microtitre plates, test tubes, and micro-centrifuge tubes.

4.7.2. Cell based assays

In addition to cell-free assays, such as described above, the readily available source of *p63* proteins provided by the present invention also facilitates the generation of cell-based assays for identifying small molecule agonists/antagonists and the like. Such assays can be used, e.g., to identify compounds which modulate expression of a *p63* gene, modulate translation of a *p63* mRNA, or which modulate the stability of a *p63* mRNA or protein. Accordingly, in one embodiment, a cell which is capable of producing *p63*, [include e.g. of cells], is incubated with a test compound and the amount of *p63* produced in the cell medium is measured and compared to that produced from a cell which has not been contacted with the test compound. The specificity of the compound vis a vis *p63* can be confirmed by various control analysis, e.g., measuring the expression of one or more control gene.

Compounds which can be tested include small molecules, proteins, and nucleic acids. In particular, this assay can be used to determine the efficacity of *p63* antisense molecules or ribozymes.

In another embodiment, the effect of a test compound on transcription of an *p63* gene is determined by transfection experiments using a reporter gene operatively linked to at least a portion of the promoter of an *p63* gene. A promoter region of a gene can be isolated, e.g., from a genomic library according to methods known in the art. The reporter gene can be any gene encoding a protein which is readily quantifiable, e.g, the luciferase or CAT gene, well known in the art.

In another embodiment, the invention provides a method for detecting functional *p63* protein in cells, preferably mammalian cells. 'functional *p63*' means a *p63* protein which is able to activate gene transcription. The invention relates to a method of determining the presence of functional *p63* based on the dependence of transactivation of certain target genes by *p63*. Examples include the *p21* gene or repair proteins for instance those activated by irradiation damage. The method comprises (a) stimulating mammalian cells to increase expression of the target MRNA; and (b) coparing the level of the MRNA in stimulated cells to the level of MRNA in unstimulated cells.

For instance, primary cultures of mammalian cells can also be used. Such cells can be biopsies taken from mammalian tumors. Mammalian cell cultures can be initiated from biopsies by surgical incisional or escisional methods. In one embodiment, the cells may be stimulated in step (a) by irradiating the cells in order to induce or stimulate expression of the repair proetins.

The RNA can be isolated from irradiated mammalian cells by methods known to those skilled in the art.

4.7.3 Ubiquitin-mediated proteolysis

Furthermore, the present invention, by making available purified and recombinant forms of the subject *p63* proteins, facilitates the development of assays that can be used to screen for drugs which inhibit the proteolysis of *p63*, such as by inhibiting ubiquitination of *p63*, or ubiquitin-mediated proteolysis of *p63*. For instance, in addition to agents which disrupt binding of *p63* to other cellular (or viral) proteins, inhibitors of ubiquitin conjugating enzymes ("E2" enzymes) or ubiquitin ligases ("E3" enzymes) may prevent transfer of ubiquitin to *p63*.

Assays for the measurement of ubiquitination can be generated in many different forms, and include assays based on cell-free systems, e.g. purified proteins or cell lysates, as well as cell-based assays which utilize intact cells. Assays as described herein can be used in conjunction with the subject *p63* proteins to generate a ubiquitin-conjugating system for detecting agents able to inhibit particular E2- or E3-mediated ubiquitination of *p63* proteins. Such inhibitors can be used, for example, in the treatment of proliferative and/or differentiative disorders, to modulate apoptosis, and in the treatment of viral infections, such by adenoviruses or papillomaviruses.

In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins or with lysates, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target. Accordingly, potential inhibitors of *p63* ubiquitination can be detected in a cell-free assay generated by consitution of a functional ubiquitin-protein ligase system in a cell lysate, such as generated by charging a reticulocyte lysate (Hersko *et al.* (1983) *J Biol Chem* 258:8206-6214) with a *p63* polypeptide and, as needed, a specific E1,

E2 or E3 enzyme (cellular or viral in origin), and ubiquitin. In an alternative format, the assay can be derived as a reconstituted protein mixture.

In yet other embodiments, the present assay comprises an *in vivo* ubiquitin-conjugating system, such as a cell able to conduct the *p63* protein through at least a portion of a ubiquitin-mediated proteolytic pathway.

The level of ubiquitination of the substrate *p63* protein brought about by the system is measured in the presence and absence of a candidate agent, and a decrease in the level ubiquitin conjugation is indicative of an inhibitory activity for the candidate agent. As described below, the level of ubiquitination of the *p63* protein can be measured by determining the actual concentration of protein:ubiquitin conjugates formed; or inferred by detecting some other quality of the subject protein affected by ubiquitination, including the proteolytic degradation of the protein. A statistically significant decrease in ubiquitination of the *p63* protein in the presence of the test compound is indicative of the test compund being, as appropriately inferred from the assay format, an inhibitor of ubiquitin conjugation to *p63* and/or ubiquitin-mediated degradation of *p63*.

In preferred *in vitro* embodiments of the present assay, the ubiquitin-conjugating system comprises a reconstituted protein mixture of at least semi-purified proteins. With respect to measuring ubiquitination, the purified protein mixture can substantially lack any proteolytic activity which would degrade the *p63* substrate protein and/or components of the ubiquitin conjugating system. For instance, the reconstituted system can be generated to have less than 10% of the proteolytic activity associated with a typical reticulocyte lysate, and preferably no more than 5%, and most preferably less than 2%. Alternatively, the mixture can be generated to include, either from the onset of ubiquitination or from some point after ubiquitin conjugation of the *p63* protein, a ubiquitin-dependent proteolytic activity, such as a purified proteosome complex, that is present in the mixture at measured amounts.

In the subject method, ubiquitin conjugating systems derived from purified proteins hold a number of significant advantages over cell lysate or wheat germ extract based assays (collectively referred to hereinafter as "lysates"). Unlike the reconstituted protein system, without knowledge of particular kinetic parameters for Ub-independant and Ub-dependent degradation of the *p63* protein in the lysate, discerning between the two pathways can be

extremely difficult. Measuring these parameters, if at all possible, is further made tedious by the fact that cell lysates tend to be inconsistent from batch to batch, with potentially significant variation between preparations. Evaluation of a potential inhibitor using a lysate system is also complicated in those circumstances where the lysate is charged with mRNA encoding the *p63* protein, as such lysates may continue to synthesize the protein during the assay, and will do so at unpredictable rates.

Using similar considerations, knowledge of the concentration of each component of the ubiquitin conjugation pathway can be required for each lysate batch, along with the degradative kinetic data, in order to determine the necessary time course and calculate the sensitivity of experiments performed from one lysate preparation to the next.

Furthermore, the lysate system can be unsatisfactory where the *p63* protein itself has a relatively short half-life, especially if due to degradative processes other than the ubiquitin-mediated pathway to which an inhibitor is sought. For example, in assays for an inhibitor of HPV-induced ubiquitination of p53, lysate based systems can be difficult to use, in addition to the reasons set forth above, due to the short half-life of p53 even in extracts which lack HPV proteins. In such systems, the ability to measure HPV-mediated ubiquitination of p53 is made difficult by the already rapid, ongoing degradation of p53 presumably occurring by proteolytic processes which are not mediated by any HPV proteins.

The use of reconstituted protein mixtures allows more careful control of the reaction conditions in the ubiquitin-conjugating system. Moreover, the system can be derived to favor discovery of inhibitors of particular steps of the ubiquitination process. For instance, a reconstituted protein assay can be generated which does not facilitate degradation of the ubiquitinated *p63* protein. The level of ubiquitin conjugated *p63* can easily be measured directly in such as system, both in the presence and absence of a candidate agent, thereby enhancing the ability to detect a inhibitor of *p63* ubiquitination. Alternatively, the Ub-conjugating system can be allowed to develop a steady state level of *p63*:Ub conjugates in the absence of a proteolytic activity, but then shifted to a degradative system by addition of purified Ub-dependent proteases. Such degradative systems would be amenable to identifying direct inhibitors of ubiquitin-mediated proteolysis of *p63*.

The purified protein mixture includes a purified preparation of the *p63* protein and ubiquitin under conditions which drive the conjugation of the two molecules. For instance,

the mixture can include a ubiquitin-activating enzyme (E1), a ubiquitin-conjugating enzyme (E2), and a nucleotide triphosphate (e.g. ATP). Alternatively, the E1 enzyme, the ubiquitin, and the nucleotide triphosphate can be substituted in the system with a pre-activated ubiquitin in the form of an E1::Ub conjugate. Likewise, a pre-activated ubiquitin can instead comprise an E2::Ub conjugate which can directly transfer the pre-activated ubiquitin to the *p63* protein substrate. Furthermore, the reconstituted mixture can also be generated to include at least one auxiliary substrate recognition protein (E3) which may be, for example, of cellular or viral origin. In illustrative embodiments described below, in order to generate an assay which approximates the ubiquitination of *p63* in HPV-16 or HPV-18 infected cells, the reconstitutated ubiquitin conjugating system may further include an E6 protein of HPV origin, as well as an E6-associated protein (E6-AP) of cellular origin.

In one embodiment of the present assay, the products of a non-degradative ubiquitin-conjugating system are separated by gel electrophoresis, and the level of ubiquitinated *p63* protein assessed, using standard electrophesis protocols, by measuring an increase in molecular weight of the *p63* protein that corresponds to the addition of one or more ubiquitin chains. For example, one or both of the *p63* protein and ubiquitin can be labeled with a radioisotope such as ^{35}S, ^{14}C, or ^{3}H, and the isotopically labeled protein bands quantified by autoradiographic techniques. Standardization of the assay samples can be accomplished, for instance, by adding known quantities of labeled proteins which are not themselves subject to ubiquitination or degradation under the conditions which the assay is performed. Similarly, other means of detecting electrophoretically separated proteins can be employed to quantify the level of ubiquitination of the *p63* protein, including immunoblot analysis using antibodies specific for either the *p63* protein or ubiquitin, or derivatives thereof. As described below, the antibody can be replaced with another molecule able to bind one of either the *p63* protein or ubiquitin. By way of illustration, one embodiment of the present assay comprises the use of biotinylated ubiquitin in the conjugating system. The biotin label is detected in a gel during a subsequent detection step by contacting the electrophoretic products (or a blot thereof) with a streptavidin-conjugated label, such as a streptavidin linked fluorochrome or enzyme, which can be readily detected by conventional techniques. Moreover, where a reconstituted protein mixture is used (rather than a lysate) as the conjugating system, it may be possible to simply detect the *p63* protein and ubiquitin

conjugates in the gel by standard staining protocols, including coomassie blue and silver staining.

In another embodiment, an immunoassay or similar binding assay, is used to detect and quantify the level of ubiquitinated *p63* protein produced in the ubiquitin-conjugating system. Many different immunoassay techniques are amenable for such use and can be employed to detect and quantitate the *p63* protein:Ub conjugates. For example, the wells of a microtitre plate (or other suitable solid phase) can be coated with an antibody which specifically binds one of either the *p63* protein or ubiquitin. After incubation of the ubiquitin-conjugated system with and without the candidate agent, the products are contacted with the matrix bound antibody, unbound material removed by washing, and ubiquitin conjugates of the *p63* protein specifically detected. To illustrate, if an antibody which binds the *p63* protein is used to sequester the protein on the matrix, then a detectable anti-ubiquitin antibody can be used to score for the presence of ubiquitinated *p63* protein on the matrix.

In similar fashion, epitope-tagged ubiquitin, such as myc-ub (see Ellison et al. (1991) *J. Biol. Chem.* 266:21150-21157; ubiquitin which includes a 10-residue sequence encoding a protein of c-myc) can be used in conjunction with antibodies to the epitope tag. A major advantage of using such an epitope-tagged ubiquitin approach for detecting Ub:protein conjugates is the ability of an N-terminal tag sequences to inhibit ubiquitin-mediated proteolysis of the conjugated *p63* protein.

Other ubiquitin derivatives include detectable labels which do not interfere greatly with the conjugation of ubiquitin to the *p63* protein. Such detectable lables can include fluorescently-labeled (e.g. FITC) or enzymatically-labeled ubiquitin fusion proteins. These derivatives can be produced by chemical cross-linking, or, where the label is a protein, by generation of a fusion protein. Several labeled ubiquitin derivatives are commercially available.

Moreover, the *p63* protein can be generated as a glutathione-S-transferase (GST) fusion protein. As a practical matter, such GST fusion protein can enable easy purification of the *p63* protein in the preparation of components of the ubiquitin-conjugating system (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel et al. (NY: John Wiley & Sons, 1991); Smith *et al.* (1988) *Gene* 67:31; and Kaelin *et al.* (1992) *Cell* 70:351) Moreover, glutathione derivatized matrices (e.g. glutathione-sepharose or glutathione-coated microtitre plates) can be used to sequester free and ubiquitinated forms of the *p63* protein

from the ubiguitin-conjugating system, and the level of ubiquitin immobilized can be measured as described. Likewise, where the matrix is generated to bind ubiquitin, the level of sequestered GST-*p63* protein can be detected using agents which bind to the GST moiety (such as anti-GST antibodies), or, alternatively, using agents which are enzymatically acted upon by GST to produce detectable products (e.g. 1-chloro-2,4-dinitrobenzene; Habig et al. (1974) *J Biol Chem* 249:7130). Similarly, other fusion proteins involving the *p63* protein and an enzymatic activity are contemplated by the present method. For example, fusion proteins containing β-galactosidase or luciferase, to name but a few, can be employed as labels to determine the amount of *p63* protein sequestered on a matrix by virtue of a conjugated ubiquitin chain.

Moreover, such enzymatic fusion proteins can be used to detect and quantitate ubiquitinated *p63* protein in a heterogeneous assay, that is one which does not require separation of the components of the conjugating system. For example, ubiquitin conjugating systems can be generated to have a ubiquitin-dependent protease which degrades the *p63* protein. The enzymatic activity of the fusion protein provides a detectable signal, in the presence of substrate, for measuring the level of the *p63* protein ubiquitination. Similarly, in a non-degradative conjugating system, ubiquitination of the *p63* protein portion of the fusion protein can allosterically influence the enzymatic activity associated with the fusion the protein and thereby provides a means for monitoring the level of ubiquitin conjugation.

In binding assay-type detection steps set out above, the choice of which of either the *p63* protein or ubiquitin should be specifically sequestered on the matrix will depend on a number of factors, including the relative abundance of both components in the conjugating system. For instance, where the reaction conditions of the ubiquitin conjugating system provide ubiquitin at a concentration far in excess of the level of the *p63* protein, (e.g., one order of magnitude or greater) sequestering the ubiquitin and detecting the amount of *p63* protein bound with the ubiquitin can provide less dynamic range to the detection step of the present method than the converse embodiment of sequestering the *p63* protein and detecting ubiquitin conjugates from the total *p63* protein bound to the matrix. That is, where ubiquitin is provided in great excess relative to the *p63* protein, the percentage of ubiquitin conjugated *p63* protein in the total ubiquitin bound to the matrix can be small enough that any diminishment in ubiquitination caused by an inhibitor can be made difficult to detect by the fact that, for example, the statistical error of the system (e.g. the noise) can be a significant

portion of the measured change in concentration of bound *p63* protein. Furthermore, it is clear that manipulating the reaction conditions and reactant concentrations in the ubiquitin-conjugating system can be carried out to provide, at the detection step, greater sensitivity by ensuring that a strong ubiquitinated protein signal exists in the absence of any inhibitor.

Furthermore, drug screening assays can be generated which do not measure ubiquitination *per se*, but rather detect inhibitory agents on the basis of their ability to interfere with binding of *p63* with any immediate upstream or downstream component of the ubiquitin conjugation or proteolysis pathways. Such assays, which are based on disrupting protein-protein interactions, can be carried out as described above for other *p63* interactors.

In still further embodiments of the present assay, the ubiquitin-conjugating system is generated in whole cells, taking advantage of cell culture techniques to support the subject assay. For example, as described below, the ubiquitin-conjugating system (including the *p63* protein and detection means) can be constituted in a eukaryotic cell culture system, including mammalian and yeast cells. Advantages to generating the subject assay in an intact cell include the ability to detect inhibitors which are functional in an environment more closely approximating that which therapeutic use of the inhibitor would require, including the ability of the agent to gain entry into the cell. Furthermore, certain of the *in vivo* embodiments of the assay, such as examples given below, are amenable to high through-put analysis of candidate agents.

The components of the ubiquitin-conjugating system, including the *p63* protein, can be endogenous to the cell selected to support the assay. Alternatively, some or all of the components can be derived from exogenous sources. In any case, the cell is ultimately manipulated after incubation with a candidate inhibitor in order to facilitate detection of ubiquitination or ubiquitin-mediated degradation of the *p63* protein. As described above for assays performed in reconstituted protein mixtures or lysate, the effectiveness of a candidate inhibitor can be assessed by measuring direct characteristics of the *p63* protein, such as shifts in molecular weight by electrophoretic means or detection in a binding assay. For these embodiments, the cell will typically be lysed at the end of incubation with the candidate agent, and the lysate manipulated in a detection step in much the same manner as might be the reconstituted protein mixture or lysate.

Indirect measurement of ubiquitination of the *p63* protein can also be accomplished by detecting a biological activity associated with the *p63* protein that is either attenuated by ubiquitin-conjugation or destroyed along with the *p63* protein by ubiquitin-dependent proteolytic processes. As set out above, the use of fusion proteins comprising the *p63* protein and an enzymatic activity are representative embodiments of the subject assay in which the detection means relies on indirect measurement of ubiquitination of the *p63* protein by quantitating an associated enzymatic activity.

Where the *p63* protein has a relatively short half-life due to ubiquitin-dependent or independent degradation in the cell, preferred embodiments of the assay either do not require cell lysis, or, alternatively, generate a longer lived detection signal that is independent of the *p63* protein's fate after lysis of the cell. With respect to the latter embodiment, the detection means can comprise, for example, a reporter gene construct which includes a positive transcriptional regulatory element that binds and is responsive to the *p63* protein. For instance, *p63* responsive elements can be used to construct the reporter gene. These can include a creatine kinase enhancer, an interleukin-6 promoter, a c-fos promoter, a β-actin promoter, an hsc70 promoter, a c-jun promoter, a p53 promoter, and a CYC1 hybrid promoter containing a p53/*p63*-binding sequence. The gene product is a detectable label, such as luciferase or β-galactosidase, or a selectable marker, such as an enzyme which confers resistance to antibiotic or other drug, and is produced in the intact cell. The label can be measured in a subsequent lysate of the cell. However, the lysis step is preferably avoided, and providing a step of lysing the cell to measure the label will typically only be employed where detection of the label cannot be accomplished in whole cells. Such embodiments of the subject assay are particularly amenable to high through-put analysis in that proliferation of the cell can provide a simple measure of inhibition of the ubiquitin-mediated degradation of the *p63* protein.

To illustrate, the plasmid pTK*luc* described in PCT Publication WO95/18974 comprises a luciferase gene whose expression is driven by the core Herpes simplex virus thymidine-kinase (TK) promoter which has been modified with either p53 (p53RE/TK), myc (mycRE/TK), or Sp1 (Sp1RE/TK) binding sites. This reporter gene construct is expected to be sensitive to the level of *p63* in the cell. For instance, When the construct lacking any of the modifications to the TK promoter is transfected into mammalian cells, the detectable luciferase activity should be low because this core TK promoter fragment does not contain

the upstream activating sequences necessary for efficient transcriptional activation of the luciferase gene by p53, and accordingly, should not be transactivated by *p63*. However transfection with the constructs in which TK is further modified to contain either 3 or 6 response-elements (RE) for one of p53, myc or Sp1, the detectable luciferase activity should increases in cells which express appropriate forms of *p63*. For example, the level of luciferase expression is significantly higher in p53-producing cells (e.g. ML1 cells) transfected with the p53RETK- containing construct than with the TK construct. Likewise, endogenous myc and Sp1 proteins can drive expression of the mycRE/TK and Sp1RE/TK constructs. As set out above, it is expected that *p63* will be degraded by the ubiquitin pathway. However, Sp1 is not known to be degraded by any ubiquitin-mediated pathway, and the SP1RE/TK construct can therefore be used as a control in the present assays. Thus, in the presence of an agent which inhibits ubiquitin-mediated degradation of *p63* in a cell harboring a p53RE/TK construct, the level of luciferase activity would increase relative to that in the cell not treated with the candidate agent.

4.8 Diagnostic and Prognostic Assays

The present methods provide means for determining if a subject is at risk for developing a disease or condition associated with disorder marked by an aberrant *p63* activity, e.g., an aberrant level of *p63* protein or particular isoform thereof. As set forth below, diseases or conditions that can be caused by an abnormal *p63* level or catalytic activity include diseases or conditions caused by or contributed to by an abnormal amount of a target peptide of *p63*.

According to a diagnostic method of the present invention, loss of the wild-type *p63* is detected. This loss may be due to either deletional and/or point mutational events. If only a single *p63* allele is mutated, an early neoplastic state is indicated. However, if both alleles are mutated then a late neoplastic state is indicated. The *p63* allele which is not deleted (i.e., that on the sister chromosome to the chromosome carrying the deletion) can be screened for point mutations, such as missense, and frameshift mutations. These mutations could lead to non-functional *p63* gene products. In addition, the point mutational events may occur in the regulatory regions, such as in the promoter of the *p63* gene, could lead to a loss or dimunition of expression of the *p63* mRNA.

In order to detect the loss of the *p63* wild-type gene in tissue, it is helpful to isolate the tissue from the surrounding normal tissues. Means for enriching tumor preparations are

known in the art, e.g., cytometry. Detection of point mutations may be accomplished by molecular cloning of the *p63* allele (or alleles) present in tumor tissue. Alternatively, the polymerase chain reaction can be used to amplify *p63* gene sequences directly from a genomic DNA preparation. The DNA sequence of the amplified sequences can be determined.

Specific deletions of the *p63* gene can also be detected. For example, restriction fragment length polymorphism (RFLP) probes for the *p63* genes may also be used to score the loss of a *p63* allele. Loss of the wild-type *p63* genes may also be detected on the basis of the loss of the wild type expression products of *p63*. Such expression products include the mRNA as well as the *p63* protein product itself.

In one embodiment, the diagnostic method comprises determining whether a subject has an abnormal mRNA and/or protein level of *p63*, such as by Northern blot analysis, reverse transcription - polymerase chain reaction (RT-PCR), *in situ* hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the method, cells are obtained from a subject and the *p63* protein or mRNA level is determined and compared to the level of *p63* protein or mRNA level in a healthy subject. An abnormal level of *p63* polypeptide or mRNA level is likely to be indicative of an aberrant *p63* activity.

In another embodiment, the diagnostic method comprises measuring at least one activity of *p63*. For example, the ability to induce transactivation of target genes, e.g. genes involved in cell cycle arrest. Comparison of the results obtained with results from similar analysis performed on *p63* proteins from healthy subjects will be indicative of whether a subject has an abnormal *p63* activity.

In preferred embodiments, the methods for determining whether a subject is at risk for developing a disease, such as a predisposition to develop tumors, associated with an aberrant *p63* activity is characterized as comprising detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of (i) an alteration affecting the integrity of a gene encoding a *p63* polypeptide, or (ii) the mis-expression of the *p63* gene. To illustrate, such genetic lesions can be detected by ascertaining the existence of at least one of (i) a deletion of one or more nucleotides from a *p63* gene, (ii) an addition of one or more nucleotides to a *p63* gene, (iii) a substitution of one or more nucleotides of a *p63* gene, (iv) a gross chromosomal rearrangement of a *p63* gene, (v) a gross alteration in

the level of a messenger RNA transcript of a *p63* gene, (vii) aberrant modification of an *p63* gene, such as of the methylation pattern of the genomic DNA, (vii) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a *p63* gene, (viii) a non-wild type level of a *p63* polypeptide, (ix) allelic loss of a *p63* gene, and/or (x) inappropriate post-translational modification of a *p63* polypeptide. As set out below, the present invention provides a large number of assay techniques for detecting lesions in a *p63* gene. These methods include, but are not limited to, methods involving sequence analysis, Southern blot hybridization, restriction enzyme site mapping, and methods involving detection of absence of nucleotide pairing between the nucleic acid to be analyzed and a probe. These and other methods are further described *infra*.

Specific diseases or disorders, e.g., genetic diseases or disorders, are associated with specific allelic variants of polymorphic regions of certain genes, which do not necessarily encode a mutated protein. Thus, the presence of a specific allelic variant of a polymorphic region of a gene in a subject can render the subject susceptible to developing a specific disease or disorder. Polymorphic regions in genes, e.g, *p63* genes, can be identified, by determining the nucleotide sequence of genes in populations of individuals. If a polymorphic region is identified, then the link with a specific disease can be determined by studying specific populations of individuals, e.g, individuals which developed a specific disease, such as hypertension. A polymorphic region can be located in any region of a gene, e.g., exons, in coding or non coding regions of exons, introns, and promoter region.

In an exemplary embodiment, there is provided a nucleic acid composition comprising a nucleic acid probe including a region of nucleotide sequence which is capable of hybridizing to a sense or antisense sequence of a *p63* gene or naturally occurring mutants thereof, or 5' or 3' flanking sequences or intronic sequences naturally associated with the subject *p63* genes or naturally occurring mutants thereof. The nucleic acid of a cell is rendered accessible for hybridization, the probe is contacted with the nucleic acid of the sample, and the hybridization of the probe to the sample nucleic acid is detected. Such techniques can be used to detect lesions or allelic variants at either the genomic or mRNA level, including deletions, substitutions, etc., as well as to determine mRNA transcript levels.

A preferred detection method is allele specific hybridization using probes overlapping the mutation or polymorphic site and having about 5, 10, 20, 25, or 30 nucleotides around the mutation or polymorphic region. In a preferred embodiment of the invention, several

probes capable of hybridizing specifically to allelic variants are attached to a solid phase support, e.g., a "chip". Oligonucleotides can be bound to a solid support by a variety of processes, including lithography. For example a chip can hold up to 250,000 oligonucleotides (GeneChip, Affymetrix). Mutation detection analysis using these chips comprising oligonucleotides, also termed "DNA probe arrays" is described e.g., in Cronin et al. (1996) Human Mutation 7:244. In one embodiment, a chip comprises all the allelic variants of at least one polymorphic region of a gene. The solid phase support is then contacted with a test nucleic acid and hybridization to the specific probes is detected. Accordingly, the identity of numerous allelic variants of one or more genes can be identified in a simple hybridization experiment.

In certain embodiments, detection of the lesion comprises utilizing the probe/primer in a polymerase chain reaction (PCR) (see, e.g. U.S. Patent Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligase chain reaction (LCR) (see, e.g., Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the *p63* gene (see Abravaya et al. (1995) *Nuc Acid Res* 23:675-682). In a merely illustrative embodiment, the method includes the steps of (i) collecting a sample of cells from a patient, (ii) isolating nucleic acid (e.g., genomic, mRNA or both) from the cells of the sample, (iii) contacting the nucleic acid sample with one or more primers which specifically hybridize to a *p63* gene under conditions such that hybridization and amplification of the *p63* gene (if present) occurs, and (iv) detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. *et al.*, 1990, Proc. Natl. Acad. Sci. USA 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. et al., 1989, Proc. Natl. Acad. Sci. USA 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. *et al.*, 1988, Bio/Technology 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In a preferred embodiment of the subject assay, mutations in, or allelic variants, of a *p63* gene from a sample cell are identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the *p63* gene and detect mutations by comparing the sequence of the sample *p63* with the corresponding wild-type (control) sequence. Exemplary sequencing reactions include those based on techniques developed by Maxim and Gilbert (*Proc. Natl Acad Sci USA* (1977) 74:560) or Sanger (Sanger et al (1977) *Proc. Nat. Acad. Sci* 74:5463). It is also contemplated that any of a variety of automated sequencing procedures may be utilized when performing the subject assays (*Biotechniques* (1995) 19:448), including sequencing by mass spectrometry (see, for example PCT publication WO 94/16101; Cohen et al. (1996) *Adv Chromatogr* 36:127-162; and Griffin et al. (1993) *Appl Biochem Biotechnol* 38:147-159). It will be evident to one skilled in the art that, for certain embodiments, the occurrence of only one, two or three of the nucleic acid bases need be determined in the sequencing reaction. For instance, A-track or the like, e.g., where only one nucleic acid is detected, can be carried out.

In a further embodiment, protection from cleavage agents (such as a nuclease, hydroxylamine or osmium tetroxide and with piperidine) can be used to detect mismatched bases in RNA/RNA or RNA/DNA or DNA/DNA heteroduplexes (Myers, *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labelled) RNA or DNA containing the wild-type *p63* sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent which cleaves single-stranded regions of the duplex such as which will exist due to base pair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After

digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton et al (1988) *Proc. Natl Acad Sci USA* 85:4397; Saleeba *et al.* (1992) Methods Enzymod. 217:286-295. In a preferred embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in *p63* cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a *p63* sequence, e.g., a wild-type *p63* sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Patent No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations or the identity of the allelic variant of a polymorphic region in *p63* genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl. Acad. Sci USA* 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; and Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control *p63* nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen *et al.* (1991) Trends Genet 7:5).

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers *et al.* (1985) Nature 313:495). When DGGE is used as

the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing agent gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner (1987) Biophys Chem 265:12753).

Examples of other techniques for detecting point mutations or the identity of the allelic variant of a polymorphic region include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation or nucleotide difference (e.g., in allelic variants) is placed centrally and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki et al. (1986) *Nature* 324:163); Saiki et al (1989) *Proc. Natl Acad. Sci USA* 86:6230). Such allele specific oligonucleotide hybridization techniques may be used to test one mutation or polymorphic region per reaction when oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations or polymorphic regions when the oligonucleotides are attached to the hybridizing membrane and hybridized with labelled target DNA.

Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation or polymorphic region of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238. In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini *et al.* (1992) *Mol. Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany (1991) *Proc. Natl. Acad. Sci USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

In another embodiment, identification of the allelic variant is carried out using an oligonucleotide ligation assay (OLA), as described, e.g., in U.S. Pat. No. 4,998,617 and in Landegren, U. *et al.*, Science 241:1077-1080 (1988). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. One of the oligonucleotides is linked to a separation marker, e.g,. biotinylated, and the other is detectably labeled. If the precise complementary sequence is found in a target molecule, the oligonucleotides will hybridize such that their termini abut, and create a ligation substrate. Ligation then permits the labeled oligonucleotide to be recovered using avidin, or another biotin ligand. Nickerson, D. A. et al. have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, D. A. *et al.*, Proc. Natl. Acad. Sci. (U.S.A.) 87:8923-8927 (1990). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA.

Several techniques based on this OLA method have been developed and can be used to detect specific allelic variants of a polymorphic region of an SR-BI gene. For example, U.S. Patent No. 5593826 discloses an OLA using an oligonucleotide having 3'-amino group and a 5'-phosphorylated oligonucleotide to form a conjugate having a phosphoramidate linkage. In another variation of OLA described in Tobe et al. ((1996)Nucleic Acids Res 24: 3728), OLA combined with PCR permits typing of two alleles in a single microtiter well. By marking each of the allele-specific primers with a unique hapten, i.e. digoxigenin and fluorescein, each OLA reaction can be detected by using hapten specific antibodies that are labeled with different enzyme reporters, alkaline phosphatase or horseradish peroxidase. This system permits the detection of the two alleles using a high throughput format that leads to the production of two different colors.

The invention further provides methods for detecting single nucleotide polymorphisms in an *p63* gene. Because single nucleotide polymorphisms constitute sites of variation flanked by regions of invariant sequence, their analysis requires no more than the determination of the identity of the single nucleotide present at the site of variation and it is unnecessary to determine a complete gene sequence for each patient. Several methods have been developed to facilitate the analysis of such single nucleotide polymorphisms.

In one embodiment, the single base polymorphism can be detected by using a specialized exonuclease-resistant nucleotide, as disclosed, e.g., in Mundy, C. R. (U.S. Pat. No.4,656,127). According to the method, a primer complementary to the allelic sequence

immediately 3' to the polymorphic site is permitted to hybridize to a target molecule obtained from a particular animal or human. If the polymorphic site on the target molecule contains a nucleotide that is complementary to the particular exonuclease-resistant nucleotide derivative present, then that derivative will be incorporated onto the end of the hybridized primer. Such incorporation renders the primer resistant to exonuclease, and thereby permits its detection. Since the identity of the exonuclease-resistant derivative of the sample is known, a finding that the primer has become resistant to exonucleases reveals that the nucleotide present in the polymorphic site of the target molecule was complementary to that of the nucleotide derivative used in the reaction. This method has the advantage that it does not require the determination of large amounts of extraneous sequence data.

In another embodiment of the invention, a solution-based method is used for determining the identity of the nucleotide of a polymorphic site. Cohen, D. et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087). As in the Mundy method of U.S. Pat. No. 4,656,127, a primer is employed that is complementary to allelic sequences immediately 3' to a polymorphic site. The method determines the identity of the nucleotide of that site using labeled dideoxynucleotide derivatives, which, if complementary to the nucleotide of the polymorphic site will become incorporated onto the terminus of the primer.

An alternative method, known as Genetic Bit Analysis or GBA ™ is described by Goelet, P. et al. (PCT Appln. No. 92/15712). The method of Goelet, P. et al. uses mixtures of labeled terminators and a primer that is complementary to the sequence 3' to a polymorphic site. The labeled terminator that is incorporated is thus determined by, and complementary to, the nucleotide present in the polymorphic site of the target molecule being evaluated. In contrast to the method of Cohen et al. (French Patent 2,650,840; PCT Appln. No. WO91/02087) the method of Goelet, P. et al. is preferably a heterogeneous phase assay, in which the primer or the target molecule is immobilized to a solid phase.

Several primer-guided nucleotide incorporation procedures for assaying polymorphic sites in DNA have been described (Komher, J. S. et al., Nucl. Acids. Res. 17:7779-7784 (1989); Sokolov, B. P., Nucl. Acids Res. 18:3671 (1990); Syvanen, A. -C., et al., Genomics 8:684-692 (1990); Kuppuswamy, M. N. *et al.*, Proc. Natl. Acad. Sci. (U.S.A.) 88:1143-1147 (1991); Prezant, T. R. *et al.*, Hum. Mutat. 1:159-164 (1992); Ugozzoli, L. *et al.*, GATA 9:107-112 (1992); Nyren, P. *et al.*, Anal. Biochem. 208:171-175 (1993)). These methods differ from GBA TM in that they all rely on the incorporation of labeled deoxynucleotides

to discriminate between bases at a polymorphic site. In such a format, since the signal is proportional to the number of deoxynucleotides incorporated, polymorphisms that occur in runs of the same nucleotide can result in signals that are proportional to the length of the run (Syvanen, A. -C., *et al.*, Amer.J. Hum. Genet. 52:46-59 (1993)).

For mutations that produce premature termination of protein translation, the protein truncation test (PTT) offers an efficient diagnostic approach (Roest, *et. al.*, (1993) *Hum. Mol. Genet.* 2:1719-21; van der Luijt, *et. al.*, (1994) *Genomics* 20:1-12). For PTT, RNA is initially isolated from available tissue and reverse-transcribed, and the segment of interest is amplified by PCR. The products of reverse transcription PCR are then used as a template for nested PCR amplification with a primer that contains an RNA polymerase promoter and a sequence for initiating eukaryotic translation. After amplification of the region of interest, the unique motifs incorporated into the primer permit sequential *in vitro* transcription and translation of the PCR products. Upon sodium dodecyl sulfate-polyacrylamide gel electrophoresis of translation products, the appearance of truncated polypeptides signals the presence of a mutation that causes premature termination of translation. In a variation of this technique, DNA (as opposed to RNA) is used as a PCR template when the target region of interest is derived from a single exon.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid, primer set; and/or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a *p63* polypeptide.

Any cell type or tissue may be utilized in the diagnostics described below. In a preferred embodiment a bodily fluid, e.g., blood, is obtained from the subject to determine the presence of a mutation or the identity of the allelic variant of a polymorphic region of an *p63* gene. A bodily fluid, e.g, blood, can be obtained by known techniques (e.g. venipuncture). Alternatively, nucleic acid tests can be performed on dry samples (e.g. hair or skin). For prenatal diagnosis, fetal nucleic acid samples can be obtained from maternal blood as described in International Patent Application No. WO91/07660 to Bianchi. Alternatively, amniocytes or chorionic villi may be obtained for performing prenatal testing.

When using RNA or protein to determine the presence of a mutation or of a specific allelic variant of a polymorphic region of a *p63* gene, the cells or tissues that may be utilized

must express the *p63* gene. Preferred cells for use in these methods include megakaryocytes, which have been shown to express the 3 zinc finger proteins of the invention (see Examples). Alternative cells or tissues that can be used, can be identified by determining the expression pattern of the specific *p63* gene in a subject, such as by Northern blot analysis.

Diagnostic procedures may also be performed *in situ* directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents may be used as probes and/or primers for such *in situ* procedures (see, for example, Nuovo, G.J., 1992, PCR *in situ* hybridization: protocols and applications, Raven Press, NY).

In addition to methods which focus primarily on the detection of one nucleic acid sequence, profiles may also be assessed in such detection schemes. Fingerprint profiles may be generated, for example, by utilizing a differential display procedure, Northern analysis and/or RT-PCR.

Antibodies directed against wild type or mutant *p63* polypeptides or allelic variant thereof, which are discussed above, may also be used in disease diagnostics and prognostics. Such diagnostic methods, may be used to detect abnormalities in the level of *p63* polypeptide expression, or abnormalities in the structure and/or tissue, cellular, or subcellular location of a *p63* polypeptide. Structural differences may include, for example, differences in the size, electronegativity, or antigenicity of the mutant *p63* polypeptide relative to the normal *p63* polypeptide. Protein from the tissue or cell type to be analyzed may easily be detected or isolated using techniques which are well known to one of skill in the art, including but not limited to western blot analysis. For a detailed explanation of methods for carrying out Western blot analysis, see Sambrook et al, 1989, supra, at Chapter 18. The protein detection and isolation methods employed herein may also be such as those described in Harlow and Lane, for example, (Harlow, E. and Lane, D., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), which is incorporated herein by reference in its entirety.

This can be accomplished, for example, by immunofluorescence techniques employing a fluorescently labeled antibody (see below) coupled with light microscopic, flow cytometric, or fluorimetric detection. The antibodies (or fragments thereof) useful in the present invention may, additionally, be employed histologically, as in immunofluorescence

or immunoelectron microscopy, for *in situ* detection of *p63* polypeptides. *In situ* detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled antibody of the present invention. The antibody (or fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the *p63* polypeptide, but also its distribution in the examined tissue. Using the present invention, one of ordinary skill will readily perceive that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve such *in situ* detection.

Often a solid phase support or carrier is used as a support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One means for labeling an anti-*p63* polypeptide specific antibody is via linkage to an enzyme and use in an enzyme immunoassay (EIA) (Voller, "The Enzyme Linked Immunosorbent Assay (ELISA)", *Diagnostic Horizons* 2:1-7, 1978, Microbiological Associates Quarterly Publication, Walkersville, MD; Voller, et al., J. Clin. Pathol. 31:507-520 (1978); Butler, Meth. Enzymol. 73:482-523 (1981); Maggio, (ed.) *Enzyme Immunoassay*, CRC Press, Boca Raton, FL, 1980; Ishikawa, *et al.*, (eds.) *Enzyme Immunoassay*, Kgaku Shoin, Tokyo, 1981). The enzyme which is bound to the antibody will react with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety which can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes which can be used to detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, alpha-glycerophosphate, dehydrogenase,

triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods which employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect fingerprint gene wild type or mutant peptides through the use of a radioimmunoassay (RIA) (see, for example, Weintraub, B., *Principles of Radioimmunoassays*, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986, which is incorporated by reference herein). The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu, or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in, which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of

luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

Moreover, it will be understood that any of the above methods for detecting alterations in a gene or gene product or polymorphic variants can be used to monitor the course of treatment or therapy.

4.9 Methods of Treating Diseases

In general, the invention provides methods for treating or preventing a disease caused by or contributed to by aberrant expression or activity of a p63 gene product, comprising administering to the subject an effective amount of a pharmaceutical composition comprising a compound which is capable of modulating a *p63* activity, such that the disease is treated or prevented in the subject. Among the approaches which may be used to ameliorate disease symptoms involving an aberrant *p63* activity are, for example, gene therapy, antisense, ribozyme, and triple helix molecules described above. Other suitable compounds include the compounds identified in the drug screening assays above, as well as the various antagonists and agonist forms of the protein.

In a preferred embodiment, the compounds of the present invention are useful for regulating tumorigensis. In fact, based on the significant nucleotide and amino acid sequence homology with p53, *p63* is a logical target for cancer therapy. The mutation spectrum of p53 provide clues to the critical functional regions of the gene, that, when mutated, contribute to the carcinogenic process. Since about 80% of the missense mutations are in the sequence-specific DNA binding midregion of the protein, investigators have focused on the transcription transactivator function of p53. However, these missense mutations and the resultant amino acid substitutions can cause aberrant protein conformations that also may alter other functional domains, including those in the carboxyl-terminus of the p53 protein. This positively charged region contains the putative major nuclear localization signal (amino acids 316-325), the oligomerization domain (amino acids 319-360), and a DNA damage-binding domain (amino acids 318-393). p53 sequence-specific DNA binding and transcriptional transactivation can also be modulated by post-translational mechanisms, including serine phosphorylation and the redox regulation of the cysteine residues responsible for binding zinc to p53. The structure-function relationship revealed by the analysis of the p53 mutation spectrum, provides us with strategies for the

development of rational cancer therapy; particularly because of the considerable sequence identity between p53 and *p63*. As discussed above, it has been observed that the sequence identity between *p63* and p73 alpha form is about 57.4% identity and the *p63* and p73 beta form shows about 69.7% identity at the protein level. *p63* alpha form and p53 exhibit 43.8% identity at the protein level.

In one embodiment, this invention is directed to the development of drugs to mimic the cell regulator function of *p63*. Strategies to screen potential drugs are suggested by the development of assays reflecting the biologic functions of the *p63* protein: its binding to specific DNA sequences, its function as a transcription factor, its function as an inducer of apoptosis, and its ability to form complexes with cellular or viral oncoproteins. For instance, in one embodiment, apoptosis, the cell death pathway may be enhanced by anticancer therapies. Cells exposed to agents that produce DNA damage, such as double-strand breaks, may use the p53/*p63*-mediated pathway to induce apoptosis. It is known in the art that certain cell growth factors act as survival factors of cancer cells, therefore, reduction of these factors would produce apoptosis, e.g., the use of anti-EGF-recptor monoclonal antibodies, which block the EGF mediated growth signal cascade, have been shown to act synergistically with anti-cancer drugs. Thus, modulating the survival factors, survival factor pathways, their cellular receptors and inhibitors provide novel methods of inhibiting tumorigeneisis. It is possible that *p63* may mediate apoptosis by both transcriptional transactivation of genes that enhance apoptosis and transcription transrepression of genes that inhibit apoptosis. These genes their encoded proteins may also be targets for therapeutic strategies.

It is known in the art that certain DNA viruses have oncoproteins that that bind to p53 and inactivate its functions, it is likely that these would also inactivate the functions of the closely analogous *p63*. The E6 protein of the oncogenic strains of the human papillomavirus binds to p53 via E6-AP, a specific ubiquitin protein ligase and enhances the digestion of p53, and possible th edigestion of *p63*. Drugs that inhibit either the formation of this protein complex or the digestion of either p53 or *p63*, might have a therapeutic benefit in tumors associated with human papillomavirus infections, such as cervical, penile, and rectal carcinomas.

p63 has been mapped to chromosome 3, i.e., 3q27. Deletions of regions of chromosome 3 have been implicated in lung, uterine, breast, testicular, and ovarian cancers, von Hippel-

Lindau and 3p deletion syndrome, renal cell and nasopharyngeal carcinomas, mesotheliomas, and various haematological malignancies. In particular, chromosomal breaks at 3q27 have been implicated in intermediate grade non-Hodgkin's lymphomas (NHL). The pathologic heterogeneity of NHL is reflected at the cellular level by the various pathways underlying NHL pathogenesis. In particular, two main categories of genetic lesions, activation of dominantly acting oncogenes and deletion of tumor-suppression genes are known in the art as contributing to lymphonogenesis. In particular, oncogene activation in NHL most commonly occurs through non-random chromosomal translocations.

In many instances, these translocations involve reciprocal exchanges between an antigen receptor locus (the immunoglobulin loci or the TCR in B- and T-cell malignancies, respectively) and various protooncogene loci. Once the protooncogne is juxtaposed to an antigen receptor locus, its expression becomes regulated by immunoglogulin TCR promoters and enhancers. The resulting transcriptional deregulation may be one factor causing activation of the translocated protooncogene. Accordingly, in one embodiment it is contemplated that overexpression of the *p63*-B forms may be implicated in NHL.

In yet another embodiment, the invention contemplates the use of a combination of strategies, for example, a low dose of a DNA damaging agent to arrest normal cells in G_1 of the cell cycle and a delayed dose of an antimitotic agent to target the mutant *p63* tumor cells that continue to progress into the S phase, G_2, and mitosis.

As observed in the case of p53, it is likely that tumor derived *p63* mutations will target amino acid residues that are important for the structural integrity of the core domain of *p63*. Failure of muatnt proteins to bind to DNA has been attributed to the structural defects in the proteins such as structural rearrangements, local unfolding of the structure, or denaturation of the core domain. Therefore, mutant *p63* can have altered sequence specific DNA-binding and function as a transcription factor either by inhibiting its transactivator activity or by changing its specificity of DNA binding and the repertoire of genes that are transcriptionally transactivated. Although, it would seem difficult to reverse mutant conformations to the wild type, numerous strategies have been considered. First, certain like p53, certain *p63* mutant proteins are believed to have temperature sensitive phenotypes, including increased transcription-transcativator and growth inhibition activities at the lower permissive temperature when compared to the non-permissive higher temperature. Second, certain peptide drugs can later the conformation of mutant *p63* in cells. Third, certain *p63* mutants

can still form tetramers and cooperate with transfected wild-type *p63* in the transcriptional tranactivation of reporter gene constructs. It would appear that *p63* missense mutants most likely to assume a wild-type protein conformation apear to be those with a substituted amino acid in the sequence specific DNA binding site. Mutations resulting in amino acid substitutions in the interior of the *p63* protein may be a thermodynamically less stable folded structure and require other strategies. Tumors having these interior *p63* mutations also bind to cellular proteins which could lead to either dominant negative or gain of oncogenic activities. Therefore, strategies such as targeting the mutant gene by triple Dna helox and antisense approaches could result in diminishing these activities and have a therapeutic benefit.

The efficacy of p53 gene therapy in human cancer cells has been demonstrated *in vitro* by Lee et al., Cancer Metastasis Rev., 14:149-61 (1995), the efficacy as xenografts in athymic nude mice has been demonstrated by Lesoon-Wood et al., Hum. Gene Ther. 6:395-405 (1995); Clayman et al., Cancer Res. 55:1-12 (1995); and Liu *et al.*, Cancer Res. 55:3117-22 (1995). The p53 gene, i.e., at p53 complementary DNA expression vector was successfully transferred any transfection or infection using either a replication defective retroviral or an adenoviral vector and tumor cell growth was inhibited. In fact, the succes of these expression vectors has led to the approval of phase I protocols in humans. In yet another embodiment, the use of the p53 complementary DNA expression vectors in gene therapy protocols is contemplated.

4.9.1. <u>Tumor Vaccines</u>

The treatment of cancer with tumor vaccines has been a goal of physicians and scientists ever since effective immunization against infectious disease with vaccines was developed. In the past, major tumor antigens had not been molecularly characterized. Recent advances are, however, beginning to
define potential molecular targets and strategies and this had evolved with the principle that T-cell mediated responses are a key target for approaches to cancer immunization. In addition, these antigens are not truly foreign and tumor antigens fit more with a self/altered self paradigm, compared to a
non-self paradigm for antigens recognized in infectious diseases. Antigens that have been used in the art include the glycolipids and glycoproteins e.g. gangliosides, the developmental

antigens, e.g., MAGE, tyrosinase, melan-A and gp75, and mutant oncogene products, e.g., p53, ras, and HER-2/neu. Vaccine possibilities include purified proteins and glycolipids, peptides, cDNA expressed in various vectors, and a range of immune adjuvants.

Yet another aspect of the present invention relates to the modification of tumor cells, and/or the immune response to tumor cells in a patient by administering a vaccine to enhance the anti-tumor immune response in a host. The present invention provides, for examples, tumor vaccines based on administration of expression vectors encoding a mutant tumor suppressor gene, e.g., p53, p73, or *p63*, or portions thereof, or immunogenic preparations of polypeptides.

In general, it is noted that malignant transformation of cells is commonly associated with phenotypic changes. Such changes can include loss, gain, or alteration in the level of expression of certain proteins. It has been observed that in some situations the immune system may be capable of recognizing a tumor as foreign and, as such, mounting an immune response against the tumor (Kripke, M., *Adv. Cancer Res.* 34, 69-75 (1981)). This hypothesis is based in part on the existence of phenotypic differences between tumor cells and normal cells, which is supported by the identification of tumor associated antigens (TAAs) (Schreiber, H., et al. *Ann. Rev. Immunol.* 6, 465-483 (1988)). TAAs are thought to distinguish a transformed cell from its normal counterpart. For example, three genes encoding TAAs expressed in melanoma cells, MAGE-1, MAGE-2 and MAGE-3, have recently been cloned (van der Bruggen, P., et al. *Science* 254, 1643-1647 (1991)). That tumor cells under certain circumstances can be recognized as foreign is also supported by the existence of T cells which can recognize and respond to tumor associated antigens presented by MHC molecules. Such TAA-specific T lymphocytes have been demonstrated to be present in the immune repertoire and are capable of recognizing and stimulating an immune response against tumor cells when properly stimulated *in vitro* (Rosenberg, S.A., et al. *Science* 233, 1318-1321 (1986); Rosenberg, S.A. and Lotze, M.T. *Ann. Rev. Immunol.* 4, 681-709 (1986)). In the case of melanoma cells both the tyrosinase gene (Brichard, V., et al. *J. Exp. Med.* 178:489 (1993)) and the Melan-A gene (Coulie et al. *J. Exp. Med.* 180:35)) have been identified as genes coding for antigens recognized by autologous CTL on melanoma cells.

Induction of T lymphocytes is a critical initial step in a host's immune response. Activation of T cells results in cytokine production, T cell proliferation, and generation of T cell-mediated effector functions. T cell activation requires an antigen-specific signal, often called a primary activation signal, which results from stimulation of a clonally-distributed T cell receptor (TcR) present on the surface of the T cell. This antigen-specific signal is usually in the form of an antigenic peptide bound either to a major histocompatibility complex (MHC) class I protein or an MHC class II protein present on the surface of an antigen presenting cell (APC). CD4+, helper T cells recognize peptides associated with class II molecules which are found on a limited number of cell types, primarily B cells, monocytes/macrophages and dendritic cells. In most cases class II molecules present peptides derived from proteins taken up from the extracellular environment. In contrast, CD8+, cytotoxic T cells (CTL) recognize peptides associated with class I molecules. Class I molecules are found on almost all cell types and, in most cases, present peptides derived from endogenously synthesized proteins. For a review see Germain, R., *Nature* 322, 687-691 (1986).

The importance of T cells in tumor immunity has several implications which are important in the development of anti-tumor vaccines. Since antigens are processed and presented before they are recognized by T cells, they may be derived from any protein of the tumor cell, whether extracellular or intracellular. In addition, the primary amino acid sequence of the antigen is more important than the three-dimensional structure of the antigen. Tumor vaccine strategies may use the tumor cell itself as a source of antigen, or may be designed to enhance responses against specific gene products. (Pardoll, D. 1993. *Annals of the New York Academy of Sciences* 690:301).

The present invention provides for various tumor vaccination methods and reagents which can be used to elicit an anti-tumor response against transformed cells which express/display a mutant *p63*, p53, or p73, or which have been engineered to present an antigen of a mutant *p63*, p53, or p73. In general, the tumor vaccine strategies of the present invention fall into two categorie: (1) strategies that use the tumor cell itself as a source of

tumor antigen, and (2) antigen-specific vaccine strategies that are designed to generate immune responses against specific antigens of mutant *p63*, p53, or p73s.

In general, a *p63*, p53, or p73 vaccine polypeptide will include at least a portion of the *p63*, p53, or p73 polypeptide including a site of mutation which, when occurring in the full-length protein, results in loss of its biological activity. Where the *p63*, p53, or p73 tumor vaccine comprises a sufficient portion of a mutant *p63*, p53, or p73 protein, the *p63*, p53, or p73 protein can be further mutated to render the vaccine polypeptide biologically inactive.

In one embodiment, a tumor cell which otherwise does not express a mutant *p63*, p53, or p73 can be rendered immunogenic as a target for CTL recognition by association of a *p63*, p53, or p73 vaccine polypeptide. For example, this can be accomplished by the use of gene transfer vectors. Such gene transfer vectors may be administered in any biologically effective carrier, e.g. any formulation or composition capable of effectively delivering the *p63*, p53, or p73 vaccine gene to cells *in vivo*. Alternatively, cells from the patient or other host organism can be transfected with the tumor vaccine construct *ex vivo*, allowed to express the *p63*, p53, or p73 protein, and, preferably after inactivation by radiation or the like, administered to an individual. In particular, viral vectors represent an attractive method for delivery of tumor vaccine antigens because viral proteins are expressed de novo in infected cells, are degraded within the cytosol, and are transported to the endoplasmic reticulum where the degraded peptide products associate with MHC class I molecules before display on the cell surface (Spooner et al. (1995) *Gene Therapy* 2:173).

Approaches include insertion of the subject gene into viral vectors including recombinant retroviruses, adenovirus, adeno-associated virus, vaccinia virus, and herpes simplex virus-1, or plasmids. Viral vectors transfect cells directly; plasmid DNA can be delivered with the help of, for example, cationic liposomes (lipofectin) or derivatized (e.g. antibody conjugated), polylysine conjugates, gramacidin S, artificial viral envelopes or other such intracellular carriers, as well as direct injection of the gene construct or $CaPO_4$ precipitation carried out *in vivo*. It will be appreciated that because transduction of

appropriate target cells represents the critical first step in gene transfer, choice of the particular gene delivery system will depend on such factors as the phenotype of the intended target and the route of administration, e.g. locally or systemically.

In addition to viral transfer methods, such as those illustrated above, non-viral methods can also be employed to cause expression of a subject *p63*, p53, or p73 polypeptide in the tissue of an animal in order to ellicit a cellular immune response. Most nonviral methods of gene transfer rely on normal mechanisms used by mammalian cells for the uptake and intracellular transport of macromolecules. In preferred embodiments, non-viral gene delivery systems of the present invention rely on endocytic pathways for the uptake of the vaccine gene by the targeted cell. Exemplary gene delivery systems of this type include liposomal derived systems, poly-lysine conjugates, and artificial viral envelopes.

In another embodiment the mutant *p63*, p53, or p73 peptides of the present invention may be directly delivered to the patient. Although such expression constructs as exemplified above have been shown to be an efficient means by which to obtain expression of peptides in the context of class I molecules, vaccination with isolated peptides has also been shown to result in class I expression of the peptides in some cases. For example, the use of synthetic peptide fragments containing CTL epitopes which are presented by class I molecules has been shown to be an effective vaccine against infection with lymphocytic choriomeningitis virus (Schultz et al. 1991. *Proc. Natl. Acad. Sci. USA* 88:2283) or sendai virus (Kast et al. 1991. *Proc Natl Acad Sci.* 88:2283). Subcutaneous administration of a CTL epitope has also been found to render mice resistant to challenge with human papillomavirus 16-transformed tumor cells (Feltkamp et al. (1993) *Eur. J. Immunol.* 23:2242-2249). It is contemplated that such peptides may be presented in the context of tumor cell class I antigens or by other, host-derived class I bearing cells (Huang et al. 1994. *Science* 264:961).

The mutant *p63*, p53, or p73 proteins, and portions thereof, may be used in the preparation of vaccines prepared by known techniques (c.f., U.S. Patents 4,565,697; 4,528,217 and 4,575,495). *p63*, p53, or p73 polypeptides displaying antigenic regions capable of eliciting protective immune response are selected and incorporated in an

appropriate carrier. Alternatively, an antitumor antigenic portion of a *p63*, p53, or p73 protein may be incorporated into a larger protein by expression of fused proteins.

The *p63*, p53, or p73 antitumor vaccines above may be administered in any conventional manner, including oranasally, subcutaneously, intraperitoneally or intramuscularly. The vaccine may further comprise, as discussed *infra*, an adjuvant in order to increase the immunogenicity of the vaccine preparation.

In some cases it may be advantageous to couple the *p63*, p53, or p73 polypeptide vaccine to a carrier, in particular a macromolecular carrier. The carrier can be a polymer to which the *p63*, p53, or p73 polypeptide is bound by hydrophobic non-covalent inneraction, such as a plastic, e.g., polystyrene, or a polymer to which the polypeptide is covalently bound, such as a polysaccharide, or a polypeptide, e.g., bovine serum albumin, ovalbumin or keyhole limpet hemocyanin. The carrier should preferably be non-toxic and non-allergenic. The *p63*, p53, or p73 polypeptide may be multivalently coupled to the macromolecular carrier as this provides an increased immunogenicity of the vaccine preparation. It is also contemplated that the *p63*, p53, or p73 polypeptide may be presented in multivalent form by polymerizing the polypeptide with itself.

In addition, the vaccine formulations may also contain one or more stabilizer, exemplary being carbohydrates such as sorbitol, mannitol, starch, sucrose, dextrin, and glucose, proteins such as albumin or casein, and buffers such as alkaline metal phosphate and the like.

The inclusion of CD4+ epitopes in the tumor vaccine in order to further enhance an anti-tumor response is also within the scope of the invention.

In other embodiments, the tumor cell itself can be used as the source of antitumor *p63*, p53, or p73 antigens. See, for review, Pardoll, D. 1993. *Annals of the New York Academy of Sciences* 690:301. For example, cells which have been identified through phenotyping as expressing a mutant *p63*, p53, or p73 can be used to generate a CTL response against a tumor. For example, tumor-infiltrating lymphocytes (TILs) may be derived from tumor biopsies which have such a phenotype. Following such protocols as described by Hom et al. (1991) *J Immunotherap* 10:153, TILs can be isolated from tumor

specimens and grown in the presence of interleukin-2 in order to generate oligoclonal populations of activated T-lymphocytes that are cytolytic to the tumor cells expressing the mutant *p63*, p53, or p73.

In other embodiments, whole cell vaccines can be used to treat cancer patients. Such vaccines can include, for example, irradiated autologous or allogenic tumor cells which express (endogenously or recombaintly) a mutant *p63*, p53, or p73 polypeptide (or fragment thereof), or lysates of such cells.

In clinical settings, the therapeutic compound of the present invention can be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system or peptide can be introduced systemically, e.g. by intravenous injection, and specific transduction of the protein in the target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the animal being quite localized. For example, the gene delivery vehicle or peptide can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g. Chen et al. (1994) *PNAS* 91: 3054-3057). A vaccine gene can be delivered in a gene therapy construct by electroporation using techniques described, for example, by Dev et al. ((1994) *Cancer Treat Rev* 20:105-115).

The pharmaceutical preparation of the vaccine therapy construct or peptide can consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g. retroviral or adenoviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system.

Suitable pharmaceutical vehicles for administration to a patient are known to those skilled in the art. For parenteral administration, the *p63*, p53, or p73 immunogen will usually be dissolved or suspended in sterile water or saline. For enteral administration, the

immunogen will be incorporated into an inert carrier in tablet, liquid, or capsular form. The preparation may also be emulsified or the active ingredient encapsulated in liposome vehicles. The composition or formulation to be administered will, in any event, contain a quantity of the *p63*, p53, or p73 polypeptide adequate to achieve the desired immunized state in the subject being treated. The immunogen preparations according to the invention may also contain other peptides or other immunogens.

Suitable carriers may be starches or sugars and include lubricants, flavorings, binders, and other materials of the same nature. For instance, the immunogen can be formulated as a pharmaceutically acceptable acid- or base-addition salt, formed by reaction with inorganic acids such as hydrochloric acid, hydrobromic acid, perchloric acid, nitric acid, thiocyanic acid, sulfuric acid, and phosphoric acid, and organic acids such as formic acid, acetic acid, propionic acid, glycolic acid, lactic acid, pyruvic acid, oxalic acid, malonic acid, succinic acid, maleic acid, and fumaric acid, or by reaction with an inorganic base such as sodium hydroxide, ammonium hydroxide, potassium hydroxide, and organic bases such as mono-, di-, trialkyl and aryl amines and substituted ethanolamines.

The immunogen, which may be coupled to a carrier, is preferably administered after being mixed with immunization adjuvants. Conventional adjuvants include, for example, complete or incomplete Freund's adjuvant, aluminum hydroxide, Quil-A, EMA, DDA, TDM-Squalene, lecithin, alum, saponin, and such other adjuvants as are well known to those in the art, and also mixtures thereof. For example, the *p63*, p53, or p73 immunogen may be mixed with the N-butyl ester (murabutide) of the muramyl dipeptide (MDP; N-acetyl-glucosamine-3-yl-acetyl-L-alanyl-D-isoglutamine) diluted in a saline solution. The mixture may then be emulsified by means of an equal volume of squalene in the presence of arlacel (excipients). It is also possible to use other adjuvants such as analogues of MDP, bacterial fractions such as streptococcal preparations (OK 432), Biostim (01K2) or modified lipopolysaccharide preparations (LPS), peptidoglycans (N-Opaca) or proteoglycans (K-Pneumonia). In the case of these excipients, water-in-oil emulsions are preferable to oil-in-water emulsions.

The use of the instant invention is predicted to be of benefit in the treatment of any type of tumor which harbors a mutant *p63*, p53, or p734 gene. For example, treatment of

tumors of the lung, breast, brain, bone, skin, bladder, kidney, ovary, or lymphocytes is contemplated. In a preferred embodiment the tumor vaccine of the present invention is used to treat melanoma.

In addition to enhancing the immune response against a tumor at its original site, the tumor cell vaccine of the current invention may also be used in a method for preventing or treating metastatic spread of a tumor or preventing or treating recurrence of a tumor. Thus, administration of modified tumor cells or modification of tumor cells *in vivo* as described herein can provide tumor immunity against cells of the original, unmodified tumor as well as metastases of the original tumor or possible regrowth of the original tumor.

Subjects develop an anti-tumor specific T cell response which is specific for mutant forms of *p63*, p53, or p73 proteins and is effective in keeping the patients disease free. Thus, the subject develops anti-tumor specific immunity. It is also contemplated that the invention may be useful in inducing immunity to tumors in susceptible individuals before they arise, for example in the case of familial malignancies. A strong hereditary component has been identified for certain types of malignancies, for example certain breast and colon cancers and in susceptability to melanoma. In families with a known susceptibility to a particular malignancy and in which one individual presently has a tumor bearing a mutant *p63*, p53, or p73 protein, peptides presented by class I molecules of these patients could be administered to susceptible, histocompatible family members to induce an anti-tumor response in the recipient against the type of tumor to which the family is susceptible. This anti-tumor response could provide protective immunity to subsequent development of a tumor in the immunized recipient.

4.9.1. Effective Dose

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining The Ld_{50} (The Dose Lethal To 50% Of The Population) And The Ed_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}.

Compounds which exhibit large therapeutic induces are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

4.9.2 Formulation and Use

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients. Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by, for example, injection, inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For such therapy, the compounds of the invention can be formulated for a variety of loads of administration, including systemic and topical or localized administration. Techniques and formulations generally may be found in Remmington's Pharmaceutical Sciences, Meade Publishing Co., Easton, PA. For systemic administration, injection is preferred, including intramuscular, intravenous, intraperitoneal, and subcutaneous. For injection, the compounds of the invention can be formulated in liquid solutions, preferably in physiologically compatible buffers such as Hank's solution or Ringer's solution. In

addition, the compounds may be formulated in solid form and redissolved or suspended immediately prior to use. Lyophilized forms are also included.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate); lubricants (e.g., magnesium stearate, talc or silica); disintegrants (e.g., potato starch or sodium starch glycolate); or wetting agents (e.g., sodium lauryl sulphate). The tablets may be coated by methods well known in the art. Liquid preparations for oral administration may take the form of, for example, solutions, syrups or suspensions, or they may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol syrup, cellulose derivatives or hydrogenated edible fats); emulsifying agents (e.g., lecithin or acacia); non-aqueous vehicles (e.g., ationd oil, oily esters, ethyl alcohol or fractionated vegetable oils); and preservatives (e.g., methyl or propyl-p-hydroxybenzoates or sorbic acid). The preparations may also contain buffer salts, flavoring, coloring and sweetening agents as appropriate.

Preparations for oral administration may be suitably formulated to give controlled release of the active compound. For buccal administration the compositions may take the form of tablets or lozenges formulated in conventional manner. For administration by inhalation, the compounds for use according to the present invention are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebuliser, with the use of a suitable propellant, e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas. In the case of a pressurized aerosol the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of e.g., gelatin for use in an inhaler or insufflator may be formulated containing a powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration bile salts and fusidic acid derivatives. in addition, detergents may be used to facilitate permeation. Transmucosal administration may be through nasal sprays or using suppositories. For topical administration, the oligomers of the invention are formulated into ointments, salves, gels, or creams as generally known in the art. A wash solution can be used locally to treat an injury or inflammation to accelerate healing.

In clinical settings, a gene delivery system for the therapeutic *p63* gene can be introduced into a patient by any of a number of methods, each of which is familiar in the art. For instance, a pharmaceutical preparation of the gene delivery system can be introduced systemically, e.g., by intravenous injection, and specific transduction of the protein in the

target cells occurs predominantly from specificity of transfection provided by the gene delivery vehicle, cell-type or tissue-type expression due to the transcriptional regulatory sequences controlling expression of the receptor gene, or a combination thereof. In other embodiments, initial delivery of the recombinant gene is more limited with introduction into the animal being quite localized. For example, the gene delivery vehicle can be introduced by catheter (see U.S. Patent 5,328,470) or by stereotactic injection (e.g., Chen et al. (1994) PNAS 91: 3054-3057). A *p63* gene, such as any one of the sequences represented in the group consisting of SEQ ID NOS 1 and 3 or a sequence homologous thereto can be delivered in a gene therapy construct by electroporation using techniques described, for example, by Dev et al. ((1994) Cancer Treat Rev 20:105-115).

The pharmaceutical preparation of the gene therapy construct or compound of the inventioncan consist essentially of the gene delivery system in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle or compound is imbedded. Alternatively, where the complete gene delivery system can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can comprise one or more cells which produce the gene delivery system.

The compositions may, if desired, be presented in a pack or dispenser device which may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

4.9.3. Kits

The invention further provides kits for use in diagnostics or prognostic methods or for treating a disease or condition associated with an aberrant *p63* protein. In one embodiment, the kit comprises a pharmaceutical composition containing an effective amount of an *p63* antagonist therapeutic and instructions for use in treating or preventing tumorigenesis. In yet another embodiment, the kit comprises a pharmaceutical composition comprising an effective amount of an *p63* agonist therapeutic.

Yet other kits can be used to determine whether a subject has or is likely to develop a disease or condition associated with an aberrant *p63* activity. Such a kit can comprise, e.g., one or more nucleic acid probes capable of hybridizing specifically to at least a portion of an *p63* gene or allelic variant thereof, or mutated form thereof.

4.10. Additional Uses for *p63* Proteins and Nucleic Acids

The *p63* nucleic acids of the invention can further be used in the following assays. The *p63* gene can also be used as a chromosomal marker in genetic linkage studies involving genes other than *p63*.

The present invention is further illustrated by the following examples which should not be construed as limiting in any way. The contents of all cited references (including literature references, issued patents, published patent applications as cited throughout this application are hereby expressly incorporated by reference. The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, Molecular Cloning A Laboratory Manual, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); DNA Cloning, Volumes I and II (D. N. Glover ed., 1985); Oligonucleotide Synthesis (M. J. Gait ed., 1984); Mullis et al. U.S. Patent No: 4,683,195; Nucleic Acid Hybridization(B. D. Hames & S. J. Higgins eds. 1984); Transcription And Translation (B. D. Hames & S. J. Higgins eds. 1984); Culture Of Animal Cells (R. I. Freshney, Alan R. Liss, Inc., 1987); Immobilized Cells And Enzymes (IRL Press, 1986); B. Perbal, A Practical Guide To Molecular Cloning (1984); the treatise, Methods In Enzymology (Academic Press, Inc., N.Y.); Gene Transfer Vectors For Mammalian Cells (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Methods In Enzymology, Vols. 154 and 155 (Wu et al. eds.), Immunochemical Methods In Cell And Molecular Biology (Mayer and Walker, eds., Academic Press, London, 1987); Handbook Of Experimental Immunology, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Manipulating the Mouse Embryo, (Cold

Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). All references cited herein are inorporated by reference in their entirety.

Exemplification

The invention now being generally described, it will be more readily understood by reference to the following examples which are included merely for purposes of illustration of certain aspects and embodiments of the present invention, and are not intended to limit the invention.

Examples

I. Identification of human and murine *p63*

It has been obsreved that the intron-exon organization was conserved between p73 and p53 (Kaghad et al., 1997), and from known exon and intron sizes for these two genes, it was possible to identify new members of this gene family using a PCR-based strategy of amplifying two exons in a conserved domain and their intervening intron. Sequence similarity in exonic regions would demonstrate a related gene, while differences in size and/or sequence or introns from p53 and p73 would indicate a novel family member. Non-degenerate and degenerate primers were designed based in sequence homology among p53 and p73 cDNAs from various species. Primers (5'-GGCCTCGAGTACAAITWCATGTGTAAYAG 27 and 5'GGCATCGATTCTCTTCCAGGGCAAGCACA), 28 designed to anneal to regions in exon 7 and exon 8, respectively, of p73 and p53, were used to amplify products from human and mouse total genomic DNA with the following conditions:

pre-PCR: 80°C 2 min, add TAQ polymerase, 94°C 5 min.
'Touchdown PCR': 94°C 1 min, 65°C 1 min,, 72°C 2 min for 3 cycles:

94° 1 min, 64°C 1 min, 72°C 2 min for 3 cycles; 94°C 1 min, 63°C 1 min, 72°C 2 min for 3 cycles; 94°C 1 min, 62°C 1 min, 72°C 2 min for 2 cycles; 94°C 1 min, 61°C 1 min, 72°C 2 min for 2 cycles; 94°C 1 min, 60°C 1 min, 72°C 2 min for 2 cycles; 94°C 1 min, 59°C 1 min, 72°C 2 min for 2 cycles; 94°C 1 min, 58°C 1 min, 72°C2 min for 20 cycles; 72°C 7 min

The above generated amplicons of approximately 800bp and 900 bp from human and mouse genomic DNA, respectively. Comparison with known sizes of the corresponding intron (7) in p73 and p53 indicated that these amplicons were derived from a novel gene that shared homology in exonic regions, as demonstrated by their ability to be generated with the above primers. The amplicons were then subcloned into a pCDNA3 or pCDNA3 or pCDNA3-GFP vector and sequenced using T7, SP6, and GFP primers. Sequence analysis confirmed homology with regions in exon 7 and exon 8 of the p73 and p53 genes, showing strong nucleotide similarity and near identity at the amino acid level, particularly to p73.

II. <u>Cloning of *p63* via Exon-bridging</u>

The recent discovery of the *p53*-related gene, *p73*, suggested that other members of the *p53* gene family exist in mammalian genomes. Given the absence of *p53*-related sequences in available expressed sequence tag (EST) libraries, it was possible that *p53*-related genes were expressed at relatively low levels or in a tissue-restricted manner, and that standard hybridization or polymerase chain reaction (PCR) approaches would be difficult. However, examination of the central portions of *p53* and *p73* showed a remarkable conservation of intron positions, while the size and sequences of these introns remained distinct between these genes (Kaghad et al., 1997; Yang et al., submitted). We therefore designed PCR primers that would anneal to regions in contiguous exons conserved between *p53* and *p73* such that the amplification product would include the intervening intron. As products from the *p53* and *p73* genes were predictable on the

basis of known intron sizes and sequence, we analyzed novel products for ones possessing terminal sequence homolocy with *p53* and *p73* bordering non-conserved intronic sequences. One primer pair designed to span intron 7 yielded an 800 basepair (bp) and 900 bp PCR product from human and mouse, respectively, genomic DNA (not shown). The ends of these products displayed sequence homology with the 3' end of exon 7 and the 5'-end of exon 8 of *p53* and *p73*, while the intervening sequence showed no homology with introns of either gene. The 800bp amplicon derived from human genomic DNA was used as a hybridization probe to screen a human PAC library, which yielded a single clone of 120Kb. Similarly, the 900bp amplicon from the mouse genomic DNA was used to isolate a single, 16.5Kb clone from a lambda DASH II murine genomic DNA phage library. Partial sequencing of exon 7 of the human and mouse genomic clones confirmed the presence of exonic sequences with similarity to those of *p53* and *p73*, and yet the presence of third base codon differences and of conserved substitutions, demonstrating that this gene was a novel member of the *p53* family.

To deduce the amino acid sequence of the protein, or proteins, encoded by this gene, we constructed a CDNA library from E15 murine embryos lacking *p73* and *p53* genes (*p73-/-*,*p53-/-*; Yang et al., unpublished results) and screened pools of the fractionated library by PCR and subsequent hybridization. Three full-length cDNAs were obtained, all of which shared a central domain with approximately 60 and 85% amino acid identity with the DNA binding domains of *p53* and *p73*, respectively (Fig. 1). Human cDNAs were deduced from sequencing reverse transcriptase-polymerase chain reaction (RT-PCR) products from the SK-N-MC neuroepithelioma cell line, and these revealed a remarkably high level of primary amino acid sequence conservation, bordering on 99%, with the mouse cDNAs (Fig. 1). Of the three murine cDNAs initially isolated, one encoded an acidic N-terminus similar to that required for transcriptional activation by *p53* and *p73*. Interestingly, the murine CDNA clone with the acidic N-terminus contains an additional 39 amino acids upstream of the methionine start site seen in human sequences to date (Fig 1, 2). These N-termini have been denoted TA* for the longer N-terminus and TA for the sequence starting with the amino acid sequence MSQ

(Fig. 1, 2). The other two murine cDNAs clones encoded proteins with a truncated N-terminus (AN) lacking the acidic, putative transactivation domain. Further transcript and cDNA analysis from both murine and human sources revealed the expression of additional variants. In total, at least six different transcripts, derived from alternative splicing events and encoding proteins with two different N-termini (TA*/TA and ΔN) and three different C-termini (α, β, and ϒ), are described (Fig.2). Partial analysis of the murine and human genes indicated that the transcripts that give rise to the truncated N-terminal proteins were derived from an alternative promoter and initiation codon in intron 3 (exon 3'; Fig. 2A). Additionally, a splicing variant in exon 9 of both species alternatively deleting four amino acids was detected in both species (not shown). To reflect the high degree of homology of the human and murine sequences to *p53* and *p73*, as well as the immense complexity of these gene products with predicted molecular weights ranging from 44,000 to 72,000 daltons, we propose that this gene be called *p63*.

To map the human *p63* gene, we employed fluorescence in situ hybridization (FISH) techniques on human metaphase chromosome spreads using the human *p63* PAC clone as a probe. The *p63* PAC clone hybridized to the long arm of chromosome 3, at approximately 3q27-29 (Fig. 3A). We also mapped the murine *p63* gene using linkage analysis, which showed that *p63* is located on the proximal portion of chromosome 16 between anonymous DNA markers D 16Mit 1 and D16Mit3 (Fig. 3B). This region is known to be syntenic with human chromosome 3q27-29, in agreement with the in situ analysis of the human *p63* gene.

Hup63geno (PAC) has since been deposited at the ATCC under the terms of the Budapest Treaty.

III. Mapping of human *p63* gene

To map the human *p63* gene, we used fluorescense in situ hybridization (FISH) on human metaphase chromosome spreads using the human *p63* PAC clone as a probe. The *p63* PAC clone hybridized to the long arm of chromosome 3 at approximately 3q27-28 (Fig. 2A). Fluorescence in situ hybridization (FISH) was performed on human

metaphase spreads using Hupo63geno (PAC) as a probe. The methods used protocols that are well known in the art. By this method, *p63* was mapped to human chromosome 3q27-29, a region implicated in various human syndromes including B-cell lymphoma and large diffuse cell lymphoma.

IV. Cloning of human *p63* cDNAs

Sequence information for human p63 transcripts were obtained by RT-PCR on total RNA isolated from the SK-B-MC cell line.

V. Cloning of murine p63 gene

The 900bp amplicon derived from mouse genomic DNA, described above, was used as a probe in hybridization screens for the murine homolog of the p63 gene. Screening of a 129 mouse genomic phage library (in lambda DASH II) yielded a clone with a 16.5 kb insert containing the murine p63 gene. Hybridization screens were done as per standard protocols, under the following conditions: prehybridization incubation (without probe) for 4 hrs at 50-55°C, in hybridization solution (50% formamide, 5X SSC, 2.5X Denhardts, 150ug/ml salmon sperm DNA, 0.1% SDS); hybridization with ^{32}P-labeled probe (in hybridization solution) for 16 hrs at 40°C; washes done in 0.5X Ssc, 0.1% SDS at 50°C. The 16.5 kb insert was released by a NotI digestion, subcloned into the pZero vector, and sequenced in its entirety. Sequence analysis showed the clone to contain a portion of the murine p63 gene, extending from intron 4 through intron 10.

VI. Cloning of murine p63 cDNAs

5' Rapid Amplification of cDNA Ends (RACE) was used to obtain further sequence information on p63 not contained within the murine genomic clone. Total RNA was isolated from c15 embryos lacking both p53 and p73, generated from mice bearing targeted mutations in both genes, and used as the template in a first stand cDNA synthesis reaction with a murine p63-specific primer (5'-GGCATCGATGAACTCACGGCTCAGCTC). An 'adapter' primer (5'-

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TTTAGTGAGGGTTAATAAGCGGCCGCGTCGTGACTGGGAGCGC) was then ligated to the cDNA product using T4 RNA ligase. PCR was subsequently performed on the ligation product using primers (5'- 31 GCCCTGGAGGCGGCCGCTTATTAACCCTCAC and 5'- 32 GGCATCGATGTAGACAGGCATGGCACG) with the conditions described in I. An approximately 610bp amplicon was generated, subcloned into pCDNA3 vector, and sequenced in its entirety. The 5'RACE product yielded a sequence corresponding to a N-terminal truncated form of murine p63.

A bacterial plasmid cDNA library was constructed from mRNA isolated from e15 embryos lacking both p53 and p73, described above, and screened for p63 cDNAs. Hybridization screens were done essentially as described in V., using a probe, corresponding to exons 5 to 9 of p63, generated by RT-PCR on total p73-/-;p53-/- mouse RNA with primers (5'-GGGCTCGAGCTGAAGAAGCTGTACTGC and 5'- 33 GGGATCGATCTCCGTTTCTTGATGGAA). Three clones were identified and sequenced in their entirety. These corresponded to three different, full-length splice variants of murine p63.

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VII. <u>Murine p63 gene targeting vector</u>

The 16.5 kb genomic fragment described in V. was used to construct a vector for targeted disruption of the p63 gene by homologous recombination in murine embryonic stem (ES) cells. Briefly, the p63 gene fragment was subcloned into the pBluescript SK(-) vector via a NotI/NarI digestion followed by ligation to compatible cohesive ends generated by a NotI/ClaI digestion of the vector plasmid. This construct, pSK-murp63geno, was then digested with SpeI and ClaI to remove a 2900bp region corresponding to portions of intron 5, all of exon 6, intron 6, exon 7, intron 7, exon 8, and portions of intron 9 (note: exon and intron designations based on exon sequence homology with p73 and p53). This region was then replaced with the neomycin

resistance gene under control of the PGK promotor (PGK-NeoR), yielding pSK-murp63genoNeo. This plasmid was then digested with SacII/NheI, removing a 2200bp fragment corresponding to a portion of intron 4 that was then replaced with the herpes simplex virus thymidine kinase gene (HSV-TK), yielding the final p63 gene targeting vector, pSK-murp63ko. This vector will be linearized and introduced into murine ES cells via electroporation. Double selection with G418 and gancyclovir, followed by DNA hybridization with external probes will identify ES clones which have under gone homologous recombination. These will then be used in blastocyst reconstitutions to generate chimeric mice bearing the targeted disruption in p63. Breeding of these chimeric mice with wildtype mice and intercrosses from subsequent F1 and F2 generations will yield mice deficient in one or both copies of the p63 gene.

VIII. Cloning of human p63 and possible novel, related genes using murine p63 cDNA

We obtained a human genomic library enriched for chromosome 22 from the ATCC and probed with a murine p63 cDNA fragment corresponding to exons 5 to 9, described in VI. Hybridizations were done as described in V, but lower stringency washes were used (5XSSC/0.1% SDS). These screens yielded one clone containing a 4 kb insert that was then subcloned into pZero vector and sequenced in its entirety. Sequence analysis showed that this clone was identical to previously obtained human p63 cDNAs in the corresponding exonic regions. This result demonstrated the ability to clone the human p63 gene using a cross-species (mouse) cDNA probe. Additional clones which yielded positive signals in our hybridization screens have been identified and will be purified and sequenced to determine if they are novel members of the p73, p63, p53 family.

IX. Immunofluorescence

Transfection of baby hamster kidney (BHK) cells with myc-epitope tagged p63 cDNAs in pCDNAA3 vector and subsequent immunofluorescence detection of protein was done essentially as described in Heald et al., 1993.

X. Expression of p63 in Human and Murine Tissues

As the *p63* cDNAs were derived from murine embryos and human cell lines, it was important to determine their expression in normal adult tissues. To address this issue, we immunized mice with bacterially-expressed glutathione-S-transferase-*p63* fusion proteins, and produced an array of monoclonal antibodies which recognize an epitope common to murine and human *p63* and ΔN-*p63* proteins (Experimental Procedures). Using one of these antibodies, the 4A4 clone, we probed paraffin sections of archival normal human tissues including foreskin, cervix, vaginal epithelium, urothelium, and prostate (Fig. 4A-D). In all of these tissues, the 4A4 monoclonal antibody showed strong nuclear staining concentrated in the basal cells of the epithelium. The predominant localization of *p63* to the basal layer of these stratified squamous and transitional epithelia is interesting in that these cells act as the progenitors of the suprabasal cells, which undergo differentiation and cell death in regenerative epithelia (Jetten and Harvat, 1997). In the prostate, the relationship between these *p63*-positive basal cells and the luminal cells is less well established, but it is thought that the basal cells are likewise the progenitors of the suprabasal, secretory cells (Myers and Grizzle, 1997).

To obtain a more extensive survey of *p63* expression in adult tissues, we prepared total RNA from various murine tissues and performed RT-PCR reactions specific for the two different *p63* N-termini, TA and ΔN. This analysis revealed the presence of transcripts encoding TA*p63* variants in heart, testis, kidney/adrenal, thymus, brain (minus cerebellum), and cerebellum (Fig. 5a). The ΔN*p63* transcript was detected in the kidney/adrenal, spleen, and thymus, but absent from the heart, liver, testis, and brain, despite the normalization of template RNA concentration in each reaction (Fig. 5B,C). This RT-PCR analysis indicated that TA*p63* and ΔN*p63* transcripts are widely expressed in adult tissues.

The immunohistochemistry on human epithelial tissues revealed high levels of *p63* expression in basal cells (Fig. 3). To determine which *p63* isotypes were expressed in these cells, RT-PCR reactions were performed on RNA prepared from primary human foreskin keratinocytes, human ectocervix, and ME180 cervical carcinoma cells. While

RNA derived from the ME180 cells yielded a positive signal in the RT-PCR reaction designed to amplify transcripts encoding the acidic N-terminus, the primary keratinocytes and the ectocervical cells showed little or no product (Fig. 5D, TA). In contrast, RNA from all three sources showed robust signals in the RT-PCR reaction designed to amplify the AN*p63* transcript (Fig. 5D, ΔN).

The analysis of RNA from primary keratinocytes indicated that the major *p63* transcripts in these cells encoded ΔN*p63* isotypes. To address this possibility at the protein level, we performed immunoblotting on protein lysates derived from human primary foreskin keratinocytes (HFK) and ME180 cervical carcinoma cells with the 4A4 monoclonal antibody. Lysates of baby hamster kidney (BHK) cells transfected with mammalian expression vectors encoding epitope-tagged *p63* isotypes were included as controls for molecular weight comparison (Fig. 5E). Significantly, the major product detected in primary keratinocytes and ME180 migrates at approximately 8okDa, slightly faster than the Myc epitope-tagged ΔN*p63α*. (Fig. 5E). The ME180 cells also express a less abundant, though detectable, product migrating at approximately 90-95kDa, similar to that of TA*p63α* (Fig. 5E). These data, taken together with the abundant ΔN*p63* RT-PCR product from the ME180 cell line and primary keratinocyte RNA, are consistent with notion that these epithelial cells predominantly express the ΔNp63α isotype.

XI. <u>Transactivation Functions of p63 Isotypes</u>

The central domain of all *p63* variants is highly homologous with the DNA binding domains of *p53* and *p73*, suggesting that at least some *p63* isotypes function as transcriptional activators. The ΔN*p63* variants, however, lack the N-terminal acidic residues thought to participate in transactivation functions of *p53* and *p73* (Ko and Prives, 1996; Levine, 1997; Kaghad et al., 1997). To determine whether any of the *p63* isotypes can act as transactivators, we tested their ability to induce expression from a reporter gene under the control of a *p53*-responsive element. Six *p63* constructs, specifically TA*p63α*, TA*p63ϒ*, ΔN*p63α*, ΔN*p63ϒ*, TA**p63α*, and TA**p63ϒ*, as well as

wildtype and mutant *p53* expression vectors, were separately expressed in Saos-2 human osteosarcoma cells, which lack endogenous *p53*, along with a β-galactosidase reporter construct containing multiple copies of a minimal *p53* binding sequence (PG- 13, Kem et al., 1992). Lysates from cells expressing wildtype *p53* yielded a strong β-galactosidase signal, while those expressing the *p53* mutant showed only a background signal (Fig. 6). Of the *p63* isotypes tested in Saos-2 cells, only TA*p63*y exhibited strong transcriptional activation of the *p53* reporter, with levels approaching 80% of that seen with *p53*. Interestingly, the TA**p63*ϒ isotype, which has a 39 amino acid N-terminal extension not found in TA*p63*ϒ, proved to be a weak transactivator in Saos-2 cells, suggesting possible regulatory elements within this additional domain. As expected, neither the ΔN*p63*ϒ nor the ΔN*p63*α variant, both of which lack the putative transctivation domain, showed strong reporter activity (Fig. 6), although the ΔN*p63*ϒ gave a low but detectable signal. Surprisingly, however, the ΔN*p63*α isotype also failed to yield a significant level of reporter gene expression, despite having the same transactivation domain as TA*p63*ϒ. A similar lack of transactivation was seen with TA**p63*α, pointing to additional regulatory facets of *p63* involving its C-terminal domain.

XII. Induction of Apoptosis by p63 Isotypes

Expression of wildtype *p53* induces apoptosis in a wide variety of cells, whereas many *p53* mutants have lost this ability (Oren, 1994). To determine whether any of the *p63* isotypes possess similar death-inducing activities, we compared the fates of baby hamster kidney (BHK) cells transfected with *p53* or *p73* vectors with those expressing *p63* isotypes. BHK cells were transfected with the *p53*, *p73*, and *p63* expression vectors and fixed 16 hours later. Cells were labeled using anti-Myc and anti-HA epitope tag antibodies to detect expressed proteins and with the DNA fluorochrome Hoechst 33278. Approximately 90% of the wildtype *p53*-expressing cells appeared raised from the substrate and showed highly condensed, lobated nuclei characteristic of apoptotic cells

(Fig. 7A). In contrast, those expressing the *p53*(V143A) mutant showed a very low percentage of apoptotic cells, despite high levels of exogenous protein expression (Fig. 7B). Cells transfected with TA*p637* proved highly vulnerable to cell death, as evidenced by nuclear morphology, despite the generally low protein levels generated from exogenous expression in these cells. However, an overexposure of the epitope-tag immunofluorescence image showed a good correspondence between apoptotic cells and TAp63ϒ expression (Fig. 7C). Curiously, cells expressing the ΔN*p63*ϒ isotype, which yielded low but measurable activity in the β-galactosidase assays (Fig 6), also exhibited a slight but noticeable level of apoptosis. The percentage of cell death induced by ΔN*p63*ϒ however, was considerably less than those seen in cells expressing *p53* or TA*p63*ϒ, despite the fact that ΔN*p63*ϒ accumulates to very high levels in BHK cells (Fig. 7D). Apoptosis was virtually absent in cells expressing high levels of either ΔN*p63α* (Fig. 7E), TA*p63α*, or TA**p63α* , consistent with the lack of transactivation seen with these variants. Finally, *p73α* and p73β exhibited little or no apoptotic activity in these cells at 16 hours, despite high levels of accumulation.

XIII. <u>ΔN-p63γ Suppresses Transactivation by p53, and Enhances that of TA-p63γ</u>

The ability of the TA*p63γ* isotype to transactivate reporter genes bearing *p53*-responsive elements suggested that, in general, *p63* isotypes can interact with *p53* DNA binding sites. As the ΔN*p63*ϒ isotypes lack the acidic N-terminus similar to that required for transcriptional activation by *p53*, it seemed feasible that such isotypes could act in a dominant-negative manner towards both *p53* and transactivating versions of *p63*, such as TA*p63*ϒ. To test whether ΔN*p63*ϒ isotypes could in fact suppress the transactivation ability of *p53*, we transfected Saos-2 cells with a constant amount wildtype *p53* and varying concentrations of either ΔN*p63*ϒ or ΔN*p63α* and assayed for transactivation of the PG-13 β-gal reporter gene. At a 5:1 DNA ratio of *p53* and ΔN*p63*ϒ transfected into Saos-2 cells,

reporter activity was reduced to 37% that of *p53* alone, while a 1:1 ratio yielded less than 20% the transactivation of *p53* (Fig. 8A). ΔN-*p63*a also showed a similar, dose-dependent inhibition of *p53* transactivation, with the higher suppressor concentration (1:1) giving near background (vector alone) levels of reporter signal (Fig. 8A).

We next asked if ΔN-*p63* isotypes could likewise affect transactivation by TAp63y. Paradoxically, cells co-transfected with TA*p63*ϒand ΔN*p63*ϒ (5: 1) yielded reporter expression slightly above that seen with TA*p63*ϒ alone (Fig. 8B). Higher levels of ΔN*p63*ϒ in the cotransfection (1:1 ratio) suppressed transactivation by TA-*p63*ϒ by a modest 20% (Fig.8B). In contrast, ΔN-*p63α* proved to be a strong suppressor of transactivation by TA*p63*ϒ, yielding only background levels of reporter signal, even when co-transfected at one-fifth the DNA concentration of TA*p63*ϒ (Fig. 8B).

Several mechanisms could underlie the ability of ΔN*p63* isotypes to suppress *p53* and *p63* in these assays. For example, given the high degree of sequence homology within the DNAbinding domains of the *p53* and *p63* proteins, it is likely that *p63* can bind *p53* DNA target sites in a competitive manner. To address this possibility, we asked whether *p63* isotypes, particularly those lacking detectable transactivation capabilities, could nonetheless interact with *p53* DNA binding sites. Electrophoretic mobility shift assays (EMSA) were performed using three separate oligonucelotides: a minimal *p53* binding sequence site (PG), a *p53* binding site in the *p2l* promoter (WAF), and a mutant *p53* binding site (MG; Kern et al., 1992) with lysates of 293 human kidney cells transfected with *p53*, ΔN*p63*ϒ, TAp63α and green fluorescent protein. *p53*, ΔN*p63*ϒ and TAp63α lysates all yielded significant shifts of both PG and WAF oligonucleotides, while GFP, included as a negative control, failed to display a similar shift (not shown). None of the lysates showed a shift of the control, non-*p53* binding oligonucleotide, MG, thus demonstrating the specificity of *p53*, ΔN*p63*ϒ and TAp63a. interactions with the *p53*-binding sites.

Another mechanism by which *p63* isotypes could affect transactivation by *p53* and *p63* is via direct protein-protein interactions, presumably through their oligomerization domains, We tested the potential for such interactions using a glutathione S-transferase (GST), TA**p63*ϒ fusion construct (GST-TA**p63*ϒ). Co-expression in BHK cells and

subsequent binding assays showed strong associations between GST-TA**p63*Υ and *p63*Υ isotypes, including ~~and~~ ΔN*p63*α but failed to reveal an interaction with *p53*.

XIV. Electrophoretic Mobility Shift Assays (EMSA)

This invention provides nucleic acids encoding a DNA binding domain of a p63 cell regulator protein. Assays for determining the location of a DNA binding domain in proteins include gel retardation assays, well known in the art. Briefly, recombinant proteins comprising various portions of a p63 cell regulator protein can be produced and their interaction with DNA can be measured by incubation with a DNA target sequence and separation of the complexes by gel electrophoresis. The DNA target sequence of a p63 cell regulator protein can be determined, e.g., by binding site selection experiments, well known in the art. Binding site selection experiments are performed by incubation of a DNA binding protein, e.g., a p63 cell regulator protein with a degenerate pool of labeled double stranded oligonucleotides and isolation of the oligonucleotides which interact specifically with the DNA binding protein. Individual oligonucleotides are then sequenced.

EMSAs were performed essentially as described in Yang, A. et al., (1998), Mol Cell 2, 305-316. Briefly, human 293 kidney cells were transfected with p53, p63, and GFP expression vectors, as indicated in Figure 25, using the calcium phosphate transfection method previously described (Heald et al., 1993, Cell 74, 463-474.; Yang et al., 1998). Cells were lysed in 150 μl detergent lysis buffer (50mM Tris pH 8, 150 mM NaCl, 0.1% Triton X-100) ~24 hrs after transfection. Lysates were then incubated for 1 hr at room temperature with 100pM ^{32}P radiolabeled, double-stranded oligonucleotides in binding buffer (16mM Hepes-KOH pH 7.5, 60 mM Kcl, 30 mM NaCl, 10% glycerol, 1mM dithiothreitol, 10 μg/ml BSA). The following oligonucleotides were used, with annealing of oligonucleotide pairs performed prior to incubation with lysate extracts above.

PG: 5'-CCTGCCTGGACTTGCCTGG + 5'-CCAGGCAAGTCCAGGCAGG. 36

35 WAF: 5'-GAACATGTCCCAACATGTTG + 5Õ-CAACATGTTGGGACATGTTC.

MG: 5'-CCTTAATGGACTTTAATGG + 5Õ-CCATTAAAGTCCATTAAGG. 38

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XV. Induction of p63 in response to UV/DNA damage

These experiments show that like p53 p63 is induced in response to stress signals such as UV-DNA damage.

RT-PCR Analysis

Total RNA was isolated from tissues and cell lines using RNAzol, dissolved in 10mM Tris pH8, 1mMEDTA (TE), and quantified using ultraviolet absorption at 260 nm. RT-PCR reactions were performed with the One-Step RT-PCR kit (Gibco-BRL), using 0.25 ug total RNA in 25 ul reactions under the following conditions: 50 °C 30 min; 94 °C 2 min; 94 °C 30 sec, 52 °C 30 sec, 72 °C 1 min for 40 cycles; 72 °C 5 min. The following primers were used: human p63 TA-specific reaction: 5' - ATGTCCCAGAGCCACACAG 41 and 5' - 42 AGCTCATGGTTGGGGCAC; human p63 ΔN-specific reaction: 5' - 43 CAGACTCAATTTAGTGAG and 5' - AGCTCATGGTTGGGGCAC 44

UV-irradiation of human keratinocytes

Human foreskin primary keratinocytes were cultured in Keratinocyte-SFM media (Gibco-BRL) and maintained in 5% CO_2. The keratinocytes were treated with 300J/m^2 UV irradiation, and harvested at times indicated for total RNA using RNAzol, as described above. RNA from untreated keratinocytes obtained from the same culture was used as a control.

Differentiation of human keratinocytes

Human foreskin primary keratinocytes were cultured in Keratinocyte-SFM media (Gibco-BRL) and maintained in 5% CO_2. To induce differentiation, Keratinocyte-SFM media was replaced with DMEM media (Gibco-BRL) containing 10% fetal bovine serum (FBS). Cells were harvested for RNA after addition of DMEM/10%FBS at times indicated. RNA from untreated keratinocytes obtained from the same culture was used as a control.

XVI. Screening for mutations of the p63 gene in human tumors and diseases.

Direct sequencing, using standard techniques, of the p63 gene will yield information on the genomic organization (i.e. intron/exon boundaries) and nucleotide sequence for exons, introns and promoter regions of p63. An important biological and diagnostic

application for these data will be to screen for sequence mutations and/or polymorphisms (including nucleotide substitutions, insertions, or deletions) that may result in a loss or gain of function of the p63 gene. These screens will employ the use of techniques standard in the field, including, but not restricted to, single strand conformation polymorphism (SSCP) analysis, and direct sequencing of DNA or RNA samples obtained from patients.

As one means of enabling this application, we have isolated a PAC clone of an approximately 120 kilobase genomic segment containing the p63 gene. Briefly, an 800bp amplicon, derived from PCR on human genomic DNA and corresponding to portions of exon 7 and 8 and intervening intron, was used as a probe in hybridization screens for the human p63 gene. Screening (done by Genome Systems) of a human genomic PAC library (made from white blood cells, male) yielded one clone containing the p63 gene. We have confirmed the identity of this PAC clone using by PCR. Hup63geno (PAC) has been deposited at the ATCC under the terms of the Budapest Treaty. The Hup63geno (PAC) clone likely contains a majority of the p63 gene, as the DNA probe used hybridizes to a core, central domain of the gene. Regardless, the sequence information, as well as the use of DNA probes derived from this PAC clone render the isolation of any portion of the p63 gene missing from this clone a standard and obvious application.

XVII. Lineage-Specific Expression of p63 in Genital Tract Neoplasia

Vulvar, cervical, endometrial, and ovarian epithelial neoplasms, mixed mullerian tumors (MMMT), stromal sarcomas and adjacent normal epithelia were studied. Serial sections were stained with monoclonal antibodies to p63 and p53. Percentages of cells staining were estimated for each neoplastic phenotype. It was found that in the vulva or cervix, p63 expression was limited to squamous epithelium and reserve cell populations. Staining was uniformly negative in benign and neoplastic endocervical glandular epithelium. Staining was weak (less than 10%) or absent in all but 2 endometrial adenocarcinomas, in all MMMTs, and in all ovarian neoplasms except one low grade transitional carcinoma. When present in adenocarcinomas, p63 staining predominated in basal/reserve type cells and foci of squamous metaplasia. P53 expression was conspicuous ($\geq 10\%$) only in endometrial

serous carcinomas (12/16), one stromal sarcoma, and one MMMT, and did not co-localize with p63.

Therefore, it appears that p63 is a unique homologue of p53 which, in the cervix, is expressed exclusively in squamous epithelium or reserve cells. In glandular lesions of other sites, p63 predominates in reserve cells, areas of squamous differentiation and basal cell populations. The sharp differences in expression of p63 between glandular and squamous epithelium, particularly in the cervix, may provide insights into the mechanisms determining phenotype in both benign and neoplastic epithelial proliferations.

XVIII. P63 is a Differentiation Specific Marker in Cervical Squamous Epithelium

The distribution of p63 expression in a range of cervical squamous epithelia was examined and contrasted it with markers for cell proliferation (Ki-67) because p63 is homologous to p53 and p53 regulation has been implicated in the pathogenesis of HPV-related squamous neoplasia.

31 biopsies classified as reactive, atrophic, intraepithelial and invasive cervical squamous epithelial alterations, as well as normal mucosa, were analyzed by immunohistochemistry for p53 and Ki-67 for distribution and correlation with morphologic phenotype. It was found that distribution of p63 closely paralleled squamous cell differentiation, staining all nuclei in the lower one third to one half of normal squamous epithelium only. Diffuse staining of all epithelial cells occurred in immature epithelia, including atrophy, immature metaplasia, immature LSILs (papillary immature metaplasia) and the immature cells of conventional low and high grade SIL and invasive cancer. In contrast, Ki-67 staining was more diffuse in neoplastic lesions, being expressed in both differentiated and undifferentiated cell nuclei, and less frequently expressed in benign processes.

Therefore, it appears that p63 is a unique homologue of p53 which, in the cervix, is expressed almost exclusively in immature squamous epithelium irrespective of the pathologic process. The morphological and immunohistochemical evidence are consistent with a role of p63 in cell differentiation, uncoupled from both cell proliferation and HPV

expression. Cessation or down-regulation of p63 expression may play a critical role in the process of squamous differentiation, both benign and neoplastic.